

FIGURE 1A

CACTGTGCGTATTGTGATGGCGCCTACGACCAGATCGGCTTCCCAACCTCGAGCTCCAA
 1-----+-----+-----+-----+-----+-----+-----+60
 GTGACACGCATAACACTACCGCGGATGCTGGTCTAGCCGAAGGGTTGGAGCTCGAGGTT
 H C A Y C D G A Y D Q I G F P N L E L Q

 GTCCACAACCTCCTGGCTCTTCTTCCCTTGGCACCGCTTCTACCTCTACTTCCACGAGAGG
 61-----+-----+-----+-----+-----+-----+-----+120
 CAGGTGTTGAGGACCGAGAAGGAACCGTGCGGAAGATGGAGATGAAGGTGCTCTCC
 V H N S W L F F P W H R F Y L Y F H E R

 ATCCTCGGAAAGCTCATAGGCGACGACACTTTCGCCCTCCCTTCTTGGAACCTGGGACGCG
 121-----+-----+-----+-----+-----+-----+-----+180
 TAGGAGCCTTTCGAGTATCCGCTGCTGTGAAAGCGGGAGGAAAGACCTTGACCCCTGCGC
 I L G K L I G D D T F A L P F W N W D A

 CCGGCGGCATGAAGCTGCCGTCGATCTACGCCGACCCCTTCGTCCTCGCTCTATGACAAG
 181-----+-----+-----+-----+-----+-----+-----+240
 GGGCCGCCGTACTTCGACGGCAGCTAGATGCGGCTGGGAAGCAGGAGCGAGATACTGTTC
 P G G M K L P S I Y A D P S S S L Y D K

 TTTCGCGACGCCAAGCACCGCCGCGAGTCTCGTCGACCTCGACTACAACGGAACCGAC
 241-----+-----+-----+-----+-----+-----+-----+300
 AAAGCGCTGCGGTTGCTGGTGGCGGTCAGGAGCAGCTGGAGCTGATGTTGCCCTTGGCTG
 F R D A K H Q P P V L V D L D Y N G T D

FIGURE 1B

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301-----+-----+-----+-----+-----+-----+-----+360
      CCTAGTTTCACCGACGACAGCAGATCGATCAGAACCTCAAGATCATGTACCGCAGGTG
      GGATCAAAGTGGCTGCGTCTCGTCTAGCTAGTCTTGGAGTTCTAGTACATGGCCGTCAC
      P S F T D A E Q I D Q N L K I M Y R Q V

361-----+-----+-----+-----+-----+-----+-----+420
      ATCTCCAACGGCAAGACGCCGTTGCTCTTCTTAGGCTCGGCTTACCGTGCCGCGACAAC
      TAGAGGTTGCCGTTCTGCGCAACGAGAAGAAATCCGAGCCGAAATGGCACGGCCGCTGTTG
      I S N G K T P L L F L G S A Y R A G D N

421-----+-----+-----+-----+-----+-----+-----+480
      CCAAAACCCCGCGGGCTCGCTCGAGAACAATACCACACGGCCCCCGTCCACGGGTGGACT
      GGTTTGGGCGCGCGCCGAGCGAGCTCTTGTATGGTGTGCCGGGCAGGTGCCACCTGA
      P N P G A G S L E N I P H G P V H G W T

481-----+-----+-----+-----+-----+-----+-----+540
      GCGACAGAAGCCCAATCTCGAGGACATGGGCAACTTCTACTCCGCGGGGCGCGAC
      CCGCTGTCTTCGGTTGGTTAGAGCTCCTGTACCCGTTGAAGATGAGGCGCCCGCGCTG
      G D R S Q P N L E D M G N F Y S A G R D

541-----+-----+-----+-----+-----+-----+-----+582
      CCTATCTTCTTCGCCCCACCATTCAAATGTCGATCGCATGTGG
      GGATAGAAGAGCGGGTGGTAAGTTTACAGCTAGCGTACACC
      P I F A H S N V D R M W

```

FIGURE 2A

```

1-----+-----+-----+-----+-----+-----+-----+-----+60
TTGCCGTTTGGAAATTGGACGCGCGCGCGCATGAAGCTGCCGTCGATCTACGCCGAC
AACGGCAAAACCTTAACCCCTGCGCGCGCGCGTACTTCGACGGCAGCTAGATGCGGCTG
L P F W N W D A P G G M K L P S I Y A D

61-----+-----+-----+-----+-----+-----+-----+-----+120
CCTTCGTCCTCGCTCTATGACAAAGTTTCGCGACGCCAAGCACCGCGCGTCTCTCGTC
GGAAGCAGGAGCGAGATACTGTTCAAAGCGCTGCGGTTTCGTGTCGGCGCCAGGAGCAG
P S S S L Y D K F R D A K H Q P P V L V

121-----+-----+-----+-----+-----+-----+-----+-----+180
GACCTCGACTACAACGGAACCGACCCCTAGTTTCACCGACGCAGAGCAGATCGATCAGAAC
CTGAGCTGATGTTGCCTTGGCTGGGATCAAAGTGGCTGCGTCTCGTCTAGCTAGTCTTG
D L D Y N G T D P S F T D A E Q I D Q N

181-----+-----+-----+-----+-----+-----+-----+-----+240
CTCAAGATCATGTACCGGCAGGTGATCTCCAACGGCAAGACGCCGTTGCTCTTCTTAGGC
GAGTCTAGTACATGCCCGTCCACTAGAGTTGCCGTTCTGCGGCAACGAGAAGAAATCCG
L K I M Y R Q V I S N G K T P L L F L G

241-----+-----+-----+-----+-----+-----+-----+-----+300
TCGGCTTACCGTGCCCGGCACAAACCCCGCGCGGCTCGCTCGAGAACATACCA
AGCCGAATGCACGGCCGCTGTTGGGTTTGGGCGCGCGCGGAGCTCTTGTATGGT
S A Y R A G D N P N P G A G S L E N I P

```

FIGURE 2B

CACGGCCCCGTCCACGGGTGGACTGGCGACAGAAAGCCAAACCAATCTCGAGGACATGGGC
301-----+-----+-----+-----+-----+-----+-----+360

GTGCCGGGGCAGGTGCCCCACCTGACCGCTGTCTTCGGTTGGGTTAGAGCTCCTGTACCCG
H G P V H G W T G D R S Q P N L E D M G

AACCTCTACTCCGGGGCGCGACCCCTATCTTCTCGCCCAACCATTCAAATGTCGATAGC
361-----+-----+-----+-----+-----+-----+-----+420

TTGAAGATGAGGCGCCCCCGCTGGGATAGAAAGCGGGTGGTAAGTTTACAGCTATCG
N F Y S A G R D P I F F A H S N V D S

ATGTGG

421----- 426

TACACC

M W

FIGURE 3A

```

1-----+-----+-----+-----+-----+-----+-----+-----+60
GTTGCTCTTCTTAGGCTCGGCTTACCGTGCCGGCGACAAACCCCGCGGGGCTC
CAACGAGAAGAAATCCGAGCCGAATGGACGGCCGCTGTTGGGTTTGGGGCCGCGCCGAG
  L  L  F  L  G  S  A  Y  R  A  G  D  N  P  N  P  G  A  G  S
61-----+-----+-----+-----+-----+-----+-----+120
GCTCGAGAACATACCACACGGCCCCCGTCCACGGTGGACTGGCGACAGAAACCAACCCAA
CGAGCTCTTGTATGGTGTGCCGGGAGGTGCCACCTGACCGCTGTCTTTGGTTGGGTT
  L  E  N  I  P  H  G  P  V  H  G  W  T  G  D  R  N  Q  P  N
121-----+-----+-----+-----+-----+-----+-----+180
TCTCGAGGACATGGGCAACTTCTACTCCGGGGGCGGACCCCTATCTTCTCGCCCCACCA
AGAGCTCCTGTACCCGTTGAAGATGAGGCGCCCGCTGGGATAGAGAAGCGGGTGGT
  L  E  D  M  G  N  F  Y  S  A  G  R  D  P  I  F  F  A  H  H
181-----+-----+-----+-----+-----+-----+-----+240
TTCAAACGTCGACCGCATGTGGTACTTGTGGAAGAAGCTCGGCGGGAAGCATCAGGACTT
AAGTTTGCAGCTGGCGTACACCATGAACACCTTCTTCGAGCCGCCCTTCGTTAGTCCCTGAA
  S  N  V  D  R  M  W  Y  L  W  K  K  L  G  G  K  H  Q  D  F
241-----+-----+-----+-----+-----+-----+-----+300
TAACGATAAGGACTGGCTCAACACCACCTTCCTCTTCTACGACGAGAATGCTGACTTAGT
ATTGCTATTCCTGACCGAGTTGTGGTGAAGGAGAAGATGCTGCTCTTACGACTGAATCA
  N  D  K  D  W  L  N  T  T  F  L  F  Y  D  E  N  A  D  L  V

```

FIGURE 3B

```
TCGAGTCACCCCTCAAGGACTGCTTGCAGCCGGAGTGGCTTCGTTACGATTACCAAGACGT
301-----+-----+-----+-----+-----+-----+-----+360
AGCTCAGTGGGAGTTCCTGACGAACGTCGGCCTCACCGAAGCAATGCTAATGGTTCTTGCA
R V T L K D C L Q P E W L R Y D Y Q D V

CGAGATCCCGTGGCTGAAGACCCGGCCGACTCCCAAGCCTTGAGGCGCAGAAACCGC
361-----+-----+-----+-----+-----+-----+-----+420
GCTCTAGGGCACCGACTTCTGGGCCGGCTGAGGGTTTCGGAACCTCCGCGTCTTTTGGCG
E I P W L K T R P T P K A L K A Q K T A

AGCGAAACACTGAAAGCTACAGACGACGCGCTTCCCGGTGACGCTGCAATCCGCGGT
421-----+-----+-----+-----+-----+-----+-----+480
TCGCTTTTGTGACTTTCGATGTCGTCTCTGCGGCAAGGCCACTGCGACGTTAGCGGCCA
A K T L K A T A E T P P F P V T L Q S A V

GAGCACGACGGTGAGGAGGCCCAAGGTATCGAGGAGCGGCAAGGAGAAGGAAGGAAGA
481-----+-----+-----+-----+-----+-----+-----+540
CTCGTGCTGCCACTCCTCCGGGTTCCATAGCTCCTCGCCGTTCCCTTCTCCTTCTCCTTCT
S T T V R R P K V S R S G K E K E E E E

GGAGGTCCTCATCGTGAGGGGATCGAGTTCGACCGCGACTACTTCATAAAGTTCGACGT
541-----+-----+-----+-----+-----+-----+-----+600
CCTCCAGGAGTAGCACCTCCCCTAGCTCAAGCTGGCGCTGATGAAGTATTTCAAGCTGCA
E V L I V E G I E F D R D Y F I K F D V
```

FIGURE 3C

```

601-----+-----+-----+-----+-----+-----+-----+-----+-----+660
      CTTCGTGAACGCCACCGAGGGTGAGGGCATCACGCCGGGGCCAGCGAGTTCGCGGGGCAG
      GAAGCACTTGCGGTGGCTCCCACTCCCGTAGTGCAGGCCCGCGGTGCGCTCAAGCGCCCGTC
          F V N A T E G E G I T P G A S E F A G S

661-----+-----+-----+-----+-----+-----+-----+-----+-----+720
      CTTCGTCAACGTCCCGCACAAAGCACACAGCACAGCAAGAAGGAGAAAGCTGAAGACGAG
      GAAGCAGTTGCAGGGCGGTGTTTCGTGTTTCGTGTCGTTCTTCCTCTTCTTCGACTTCTGCTC
          F V N V P H K H K H S K K E K K L K T R

721-----+-----+-----+-----+-----+-----+-----+-----+-----+780
      GCTCTGCCTGGGGATCACTGACCTGCTCGAGGACATCGGGGGGAGGACGACGACAGCGT
      CGAGACGGACCCCTAGTAGCTGGACGAGCTCCTGTAGCCCCCGCCTCCTGCTGCTGTCGCA
          L C L G I T D L L E D I G A E D D S V

781-----+-----+-----+-----+-----+-----+-----+-----+-----+840
      GCTCGTCACCATCGTCCCGAAAGCCGAAAGGCAAGGTGTCGGTCGCCGGCCTCCGCAT
      CGAGCAGTGGTAGCAGGGCTTTTCGGCCTTTCCCGTTCCACAGCCAGCGGCCGGAGCGTA
          L V T I V P K A G K G K V S V A G L R I

841-----+-----+-----+-----+-----+-----+-----+-----+-----+900
      CGATTTCCCAAATTGAAGTAATACTATATATTTCTACTACCTATCAAGGAAATAAAAGC
      GCTAAAGGGTTTAACTTCACTTATGATATATAAAGATGATGGATAGTTCCTTTATTTTCG
          D F P N * S N T I Y F Y Y L S R K I K A

      CGCACCATCGTAACAAAAA
901-----+-----+-----+-----+-----+-----+-----+-----+-----+925
      GCGTGGTAGCATTTGTTTTTTTTT
          A P S * Q K K K

```

FIGURE 4A

```

GTTGCTCTTCTTAGGCTCGGCTTACCGTGCCGGTGACCAAGCCTAACCCCGCGCGGGATC
1-----+-----+-----+-----+-----+-----+-----+60
CAACGAGAAAGATCCGAGCCGAATGCCACGGCCACTGGTCGGATTGGGGCCGCGCCCTAG
  L L F L G S A Y R A G D Q P N P G A G S

CATCGAGAACATGCCGCACAAACAGTGCACTTGTGGACCGGCGACCCAGCCCA
61-----+-----+-----+-----+-----+-----+-----+120
GTAGCTCTTGTACGGCGTGTGTTGCACGTGAACACCTGGCCGCTGGCGTGGTCCGGTT
  I E N M P H N N V H L W T G D R T Q P N

CTTCGAGAACATGGGCACCTTCTACGGCGGCGCGCACCCCATCTTCTTCGCCCA
121-----+-----+-----+-----+-----+-----+-----+180
GAAGCTCTTGTACCCGTGGAAGATGCGCCGCGCGCTGGGGTAGAAGACGGGTGGT
  F E N M G T F Y A A A R D P I F F A H H

CGCCAACATCGACCCGAATGTGGTACCTGTGGAAGAAGCTCAGCAGGAAGCACCGACTT
181-----+-----+-----+-----+-----+-----+-----+240
GCGGTTGTAGCTGGCTTACACCATGGACACCTTCTTCGAGTCGTCCCTTCGTGGTCCGAA
  A N I D R M W Y L W K K L S R K H Q D F

CAATGACTCGGACTGGCTCAAAGCTTCTTCCTCTTCTACGACGAGAACCGGACTTAGT
241-----+-----+-----+-----+-----+-----+-----+300
GTTACTGAGCCTGACCGAGTTTCGAAGGAAGGAGAAGATGCTGCTCTTGGCGCTGAATCA
  N D S D W L K A S F L F Y D E N A D L V

```


FIGURE 4B

```

TCGGGTACGGTCAAGGACTGCTTGAGACCGAGTGGCTGCGCTACACGTACCAAGACGT
301-----+-----+-----+-----+-----+-----+-----+360
AGCCCAGTGCCAGTTCTGTACGAACCTCTGGCTCACCGACGCGGATGTGCATGGTTCTGCA
    R V T V K D C L E T E W L R Y T Y Q D V

GAAGATCCCATGGGCGAACAACCCGACCGACTCCCAAGCTCGCAAGCGAGGAAAGCCGG
361-----+-----+-----+-----+-----+-----+-----+420
CTTCTAGGGTACCCGCTTGTGGGCTGGCTGAGGGTTCGAGCGGTTCCGCTCCTTTCGGCC
    K I P W A N T R P T P K L A K A R K A G

CAGCAGATCGCTGAAAGCCACCGCGGAGGTGCAGTTCCTGTGACGCTGGAATCCCCGGT
421-----+-----+-----+-----+-----+-----+-----+480
GTCGTCTAGCGACTTTCGGTGGCGCCTCCACGTCAAGGACACTGCGACCTTAGGGCCA
    S R S L K A T A E V Q F P V T L E S P V

CAAAGTGACGGTGAAGAGGCCCAAGTGGGAGGAGCGGCAAGGAGAAGGAAATGAGGA
481-----+-----+-----+-----+-----+-----+-----+540
GTTTCACTGCCACTTCTCCGGGTTCACCCCTCCTCGCCGTTCTCCTTCTACTCCT
    K V T V K R P K V G R S G K E K E D E E

GGAGATACTCATAGTGAGGGGATCGAGTTCGACCGGACTACTTCATCAAGTTCGACGT
541-----+-----+-----+-----+-----+-----+-----+600
CCTCTATGATATCACCTCCCCCTAGCTCAAGCTGGCGCTGATGAAGTAGTTCAAGCTGCA
    E I L I V E G I E F D R D Y F I K F D V

```

FIGURE 4C

```

CTTCGTGAACGCGACGGAGGCGGACGGCATCACGGCCGGGCCAGTGAGTTCGCCGGCAG
601-----+-----+-----+-----+-----+-----+-----+660
GAAGCACTTGCGCTGCCCTCCCGCTGCCGTAAGTCCCGGCCCGGTCACCTCAAGCGGCCGTC
    F V N A T E G D G I T A G A S E F A G S
CTTCGTGAACGTCCCGCACAGCACAGCACCGCAAGGATGAGAATAAGCTGAAGACGAG
661-----+-----+-----+-----+-----+-----+-----+720
GAAGCACTTGCAAGGCGGTTCGTGTTTCGTGGCGTTCCTACTCTTATTCGACTTCTGCTC
    F V N V P H K H K H R K D E N K L K T R
GCTGTGCTGTGGGAATCACCGACCTGCTCGAGGACATCGGCGCGGAGACGACGACGCGT
721-----+-----+-----+-----+-----+-----+-----+780
CGACACAGACCCCTTAGTGGCTGGACGAGCTCCTGTAGCCGCGCCTCCTGCTGTGCTCGCA
    L C L G I T D L L E D I G A E D D S V
GCTCGTCACCATCGTGCCGGAAGGCGAGGCAAGAAAGGTGTCCGTGCGCGGTCTTCGGAT
781-----+-----+-----+-----+-----+-----+-----+840
CGAGCAGTGGTAGCACGGCTTCCGTCCGTTTCCCTTTCCACAGCGACGCCGAGAACCTTA
    L V T I V P K A G K G K V S V G G L R I
TGACTTTTCCAAGTGAGGAAATAAAAGAAATTCACGTGCCGTGCCCTGCTTCAATGTACGA
841-----+-----+-----+-----+-----+-----+-----+900
ACTGAAAAGGTTCACTCCTTTATTTCTTAAGTGACGGCACGGACGAAAGTTACATGCT
    D F S K * G N K R I H V P C L L S M Y E
ATAAAATAAGAGTGTCATCATCACCGACCATGGTTCTACTTTAAAAAATAAAAAAATAAAA
901-----+-----+-----+-----+-----+-----+-----+960
TATTTTATCTCAGCTAGTAGTGGCTGGTACCAAGATGAAATTTTTTTTTTTTTTTTTT
    * N K S A S S P T M V L L * K K K K K

```

FIGURE 5A

```

1-----+-----+-----+-----+-----+-----+-----+-----+-----+60
GATCCGACGTTTGGCGTTGCCATATTGGAACCTGGGATCATCCAAGGGCATGCGTTTGCCA
CTAGGCTGCAAAACGCAACGGTATAACCTTGACCCTAGTAGGTTTCCCGTACGCAAAACGGT
D P T F A L P Y W N W D H P P K G M R L P

61-----+-----+-----+-----+-----+-----+-----+-----+-----+120
CACATGTTTGATCAACCAACGCTGTACCCCTGATCTTTACGATCCAAGACGTAAACCAAGAA
GTGTACAAACTAGTTGGTTTGACACATGGGACTAGAAATGCTAGGTTCTGCATTTGGTTCTT
H M F D Q P P N V Y P D L Y D P R R N Q E

121-----+-----+-----+-----+-----+-----+-----+-----+-----+180
CACC GCGGTTCTGTAATCATGGACCTTGGTCATTTTGGTCAAGACGTGAAAGGAACTGAC
GTGGCGCCAAGACATTAGTACCTGGAACCAAGTAAACCAGTTCTGCACCTTTCCTTGACTG
H R G S V I M D L G H F G Q D V K G T D

181-----+-----+-----+-----+-----+-----+-----+-----+-----+240
TTGCAAAATGATGAGCAATAACCTTACTCTAATGTATCGTCAAAATGATTACCAATTCCACCA
AACGTTTACTACTCGTTATTGGAATGAGATTACATAGCAGTTTACTAATGGTTAAGTGGT
L Q M M S N N L T L M Y R Q M I T N S P

241-----+-----+-----+-----+-----+-----+-----+-----+-----+300
TGTCACAACCTCTTTTTCGGTAAGCCATATTGTACGGAAGTTGGACCCCAACCAAGGCAG
ACAGGTGTTGAGAAAAAGCCATTTCGGTATAACATGCCTTCAACCTGGGTTTGGTCCCGTC
C P Q L F F G K P Y C T E V G P K P G Q

```

FIGURE 5B

GGAGCTATTGAAAAACATCCCTCATACTCCTGTCCACATTTGGGTTGGTAGTAAGCCTAAT
301-----+-----+-----+-----+-----+-----+-----+360

CCTCGATAACTTTTGTAGGGAGTATGAGGACAGGTGTAACCCCAACCATCATTCGGATTA
G A I E N I P H T P V H I W V G S K P N

GAGAACTAACTGTAAAAACGGTGAAGATATGGGAAATTTCTATTTCAGCTGGTAAGGATCCT
361-----+-----+-----+-----+-----+-----+-----+420

CTCTTATTGACATTTTGGCCACTTCTATACCCCTTTAAAGATAAGTCGACCATTCCTAGGA
E N N C K N G E D M G N F Y S A G K D P

GCCTTCTATAGTCACCATGCAAAATGTAGATCGCATGTGGACAATATGGAAAAACATTAGGA
421-----+-----+-----+-----+-----+-----+-----+480

CGAAAGATATCAGTGGTACGTTTACATCTAGCGTACACCTGTTATACCTTTTGTAAATCCT
A F Y S H H A N V D R M W T I W K T L G

GGAAAAACGCAAGGACATCAACAAGCCAGATTATTTGAACACTGAGTTCTTTTCTACGAC
481-----+-----+-----+-----+-----+-----+-----+540

CCTTTTGGGTTCCCTGTAGTTGTTTCGGTCTAATAAACTTGACTCAAGAAAAAGATGCTG
G K R K D I N K P D Y L N T E F F F Y D

GAAAA

541----- 545

CTTTT

E

FIGURE 6A

```

1-----+-----+-----+-----+-----+-----+-----+-----+60
TGCACGTGTCGTATTGCAACGGTGCTTACAAAATTGGTGGCAAAGAGTTACAAGTCCATT
ACGTGACACGCATAACGTTGCCACGAATGTTTAAACCACCGTTTCTCAATGTTCAGGTAA
  H C A Y C N G A Y K I G G K E L Q V H F

61-----+-----+-----+-----+-----+-----+-----+-----+120
TCTCGTGGCTTTTTCCTTTTTCATAGATGGTACTTGTACTTCTATGAAAGAATCTTGG
AGAGACCCGAAAAAAGGAAAAGTATCTACCATGAACATGAAGATACTTCTTAGAACC
  S W L F F P F H R W Y L Y F Y E R I L G

121-----+-----+-----+-----+-----+-----+-----+-----+180
GCTCTTAAATGATCCTACTTTTGGTTTGCCATATTGGAAC TGGGACCATCCAAAGG
CGAGAAATTAATTACTAGGATGAAACCAACGGTATAACCTTGACCCCTGGTAGGTTCC
  S L I N D P T F G L P Y W N W D H P K G

181-----+-----+-----+-----+-----+-----+-----+-----+240
GCATGCGTATACCTCCCATGTTTCGATCGTGAAGGTCCTTCCCTTTACGACGAAAAACGTA
CGTACGCATATGGAGGGTACAAGCTAGCACTTCCCAGAAAGGGAATGCTGCTTTTTCAT
  M R I P P M F D R E G S S L Y D E K R N

241-----+-----+-----+-----+-----+-----+-----+-----+300
ACCAAAGTCACCGTAATGGAACCATAATTGATCTTGGTCATTTCCGGTCAAGAAGTCCAAA
TGGTTTCAGTGGCATTAACCTTGGTATTAACTAGAACCAAGTAAAGCCAGTTCTTCAGGTTT
  Q S H R N G T I I D L G H F G Q E V Q T

```

FIGURE 6B

CAACTCAACTGCAGCAGATGACTAATAACTTAATAATGTATCGTCAAAATGATAACTA
301-----+-----+-----+-----+-----+-----+-----+360
GTTGAGTTGACGTCGTCCTACTGATTATTGAATTGATATTACATAGCAGTTTACTATTGAT
T Q L Q Q M T N N L T I M Y R Q M I T N
ATGCTCCTTGCCCCCTTGCTCTTCTTTGGTCAGCCTTACCCTCTAGGAACCTGATCCCAGTC
361-----+-----+-----+-----+-----+-----+-----+420
TACGAGGAACGGGGAACGAGAAGAAACCAGTCGGAATGGGAGATCCTTGACTAGGGTCAG
A P C P L L F F G Q P Y P L G T D P S P
CAGGGATGGGCACCTATTGAAAACATCCCTCATACTCCTGTCCACATTTGGTTGGTAGTA
421-----+-----+-----+-----+-----+-----+-----+480
GTCCCTACCCGTGATAACTTTTGTAGGGAGTATGAGGACAGGTGTAAACCCCAACCATCAT
G M G T I E N I P H T P V H I W V G S R
GGCTTGATGAGAATAATACGAAACACGGTGAGGATATGGGTAATTTTACTCGGCCGGTT
481-----+-----+-----+-----+-----+-----+-----+540
CCGAAC TACTCTTATTATGCTTTGTGCCACTCCTATACCCATTAATAAATGAGCCGGCCAA
L D E N N T K H G E D M G N F Y S A G L
TAGACCCGCTTTTCTATTCCCATCACGCCCAATGTGGACCCGGATGTGGTCCGAGTGGAAG
541-----+-----+-----+-----+-----+-----+-----+600
ATCTGGCGGAAAAGATAAGGGTAGTGCGGTTACACCTGGCCTACACGAGCTCACCTTTC
D P L F Y S H H A N V D R M W S E W K A

FIGURE 6C

```

CCTTAGGAGGAAAGGATCTCACGCACAAAGATTGGTTGAACTCCGAGTTCCTTT
601-----+-----+-----+-----+-----+-----+660
GGAATCCTCCCTTTTCTCCCTAGAGTGCCTGTTTCTAACCAACTTGAGGCTCAAGAAA
    L  G  G  K  R  R  D  L  T  H  K  D  W  L  N  S  E  F  F  F
TCTACGATGAAAA
661-----+----- 673
AGATGCTACTTTT
    Y  D  E
```

FIGURE 7A

```

1  TGCATTGTGCGTATTGCAACGATGCTTACACAATGGGTGACCAAAAAGTTACAAGTTCACC
   +-----+-----+-----+-----+-----+-----+-----+-----+
2  ACGTAACACGCATAACGTTGCTACGAATGTGTACCCACTGGTTTCAATGTTCAAGTGG
   H C A Y C N D A Y T M G D Q K L Q V H Q
61 AATCGTGGCTTTTCTTCCCGTTTCATAGATGGTACTTGTACTTCTACGAGAGAATCTTGG
   +-----+-----+-----+-----+-----+-----+-----+-----+
62 TTAGCACCGAAAGAAGGGCAAGTATCTACCATGAACATGAAGATGCTCTCTTAGAACC
   S W L F F P F H R W Y L Y F Y E R I L G
121 GCTCCCTCATCGATGATCCAACTTTTGTCTCTGCCATATTGGAACCTGGACCATCCAAGCG
   +-----+-----+-----+-----+-----+-----+-----+-----+
122 CGAGGGAGTAGCTACTAGGTTGAAAACGAGACGGTATAACCTTGACCCCTGGTAGGTTGCG
   S L I D D P T F A L P Y W N W D H P S G
181 GCATGCGTTTGCCCTGCTATGTTTCGATGTCGAAGGTTCTTCCCTCTACGATGCAAGACGTA
   +-----+-----+-----+-----+-----+-----+-----+-----+
182 CGTACGCAAACGGACGATACAAGCTACAGCTTCCAAGAAGGGAGATGCTACGTTCTGCAAT
   M R L P A M F D V E G S S L Y D A R R N
241 ATCCACATGTCCGTAATGGAACCATAATCGATCTTGGTTTTTTCGGTGATGAAGTCAAAA
   +-----+-----+-----+-----+-----+-----+-----+-----+
242 TAGGTGTACAGGCATTACCTTGGTATTAGCTAGAACCAAAAAGCCACTACTTCAAGTTT
   P H V R N G T I I D L G F F G D E V K T

```


FIGURE 7B

301-----+-----+-----+-----+-----+-----+-----+360
 CTAATGAAATACAGATGATAACTAACTTAATTCTAATGTATCGTCAAAATGATAACTA
 GATTACTTTATGTCTACTATTGATTGTTGAATTAAGATTACATAGCAGTTTACTATTGAT
 N E I Q M I T N N L I L M Y R Q M I T N

 361-----+-----+-----+-----+-----+-----+-----+420
 ATGCTCCATGCCCGCTGTTGTTCTTCGGAGAGCCTTACAGATTCCGGATCTAAACCCAATC
 TACGAGGTACGGGCGACAACAAGAAGCCCTCTCGGAATGTCTAAGCCTAGATTTGGGTTAG
 A P C P L L F F G E P Y R F G S K P N P

 421-----+-----+-----+-----+-----+-----+-----+480
 CGGGGCAGGAACCATTGAAAACATTCCCTCATACTCCGGTTCACATTTGGACTGGTACTG
 GCCCCGTCCTTGGTAACCTTTTGTAAGGAGTATGAGGCCAAGTGTAACCTGACCATGAC
 G Q G T I E N I P H T P V H I W T G T V

 481-----+-----+-----+-----+-----+-----+-----+540
 TCGCGTGACGGATTGGGTAATTGTGTGCCATCATACGGTGAGGATATGGTAATTCT
 ACGCCACATGCCCTAAACCCATTAAACACACGGTAGTATGCCACTCCTATACCCATTAAAGA
 R C T D L G N C V P S Y G E D M G N F Y

 541-----+-----+-----+-----+-----+-----+-----+600
 ACTCAGCTGGTTTAGACCCAGTTTTTTACAGCCACCACGCCAATGTGGACCGCATGTGGA
 TGAGTCGACCAAAATCTGGGTCAAAAATGTCTGGTGTGGGTACACCTGGCGTACACCT
 S A G L D P V F Y S H H A N V D R M W N

FIGURE 7C

```
601-----+-----+-----+-----+-----+-----+660
      ATGAATGGAAAGCACTAGGAGGGGAAAAGAGGGATCTCACAGACAATGATTGGTTAAACT
      TACTTACCTTTTCGTGATCCTCCCTTTTCTTCCCTAGAGTGCTGTACTAACCAATTGA
      E W K A L G G K R R D L T D N D W L N S

      CGGAGTTCCTTTTCTACGACGAAAA
661-----+-----+-----+-----+-----+-----+685
      GCCTCAAGAAAAAGATGCTGCTTTT
      E F F F Y D E
```

FIGURE 8A

```

TGCATTGTGCGTACTGCGACGGCGGTATGACCAAAATCGGCTTCCCCGATCTCGAGATCC
1-----+-----+-----+-----+-----+-----+-----+-----+60
ACGTAACACGCATGACGCTGCCGCGCATACTGGTTAGCCGAAGGGCTAGAGCTCTAGG
      H C A Y C D G A Y D Q I G F P D L E I Q

AGATCCACAACCTCGTGGCTCTTCTTCCCTTGGCACCGGTTCTACCTCTACTTCAACGAGC
61-----+-----+-----+-----+-----+-----+-----+-----+120
TCTAGGTGTTGAGCACCGAGAAAGAAAGAACCGTGGCCCAAGATGGAGATGAAGTTGCTCG
      I H N S W L F F P W H R F Y L Y F N E R

GCATACTCGGGAAACTTATCGGCGACGACACGTTGCGGCTGCCCTTCTGGAACCTGGGACG
121-----+-----+-----+-----+-----+-----+-----+-----+180
CGTATGAGCCCTTTGAATAGCCGCTGCTGTGCAAGCGCGACGGAAGACCTTGACCCCTGC
      I L G K L I G D D T F A L P F W N W D A

CGCCGGGGGCATGCAGTTCCCGTCTATCTACACGGACCCCTTCATCCTCGCTATATGACA
181-----+-----+-----+-----+-----+-----+-----+-----+240
GCGGCCCCCGTACGTCAAGGGCAGATAGATGTGCCCTGGGAAGTAGGAGCGATATACTGT
      P G G M Q F P S I Y T D P S S S L Y D K

AGCTGCGTGATGCGAAGCACCAAGCCGCCGACTTTGATTGACCTCGACTACAATGACCCG
241-----+-----+-----+-----+-----+-----+-----+-----+300
TCGACGCACTACGCTTCGTGGTGGCGGCTGAAACTGAACTGAGAGCTGATGTACCGTGGC
      L R D A K H Q P P T L I D L D Y N G T D

```

FIGURE 8B

```

301-----+-----+-----+-----+-----+-----+-----+-----+360
      ATCCTACCTTCTCCCTGAAGAACAGATTAAACCACAACCTCGCCGTCATGTACCGACAGG
      TAGGATGGAAGAGGGGACTTCTTGTCTAATTGGTGTGGAGCGGCAGTACATGGCTGTCC
          P T F S P E E Q I N H N L A V M Y R Q V

      TGATATCCAGTGGAAAGACACACAGAGCTGTTTATGGGCTCAGCGTACCGCGCCGGTGACC
361-----+-----+-----+-----+-----+-----+-----+-----+420
      ACTATAGGTCACCTTTCTGTGGTCTCGACAAATACCCGAGTCGCTGCGCGGCCCACTGG
          I S S G K T P E L F M G S A Y R A G D Q

      AGCCTGACCCCGCGCAGGTTCTGTAGAGCAGAAGCCGCACGGCCCCGGTGCTGTGGA
421-----+-----+-----+-----+-----+-----+-----+-----+480
      TCGGACTGGGGCCCGTCCAAGACATCTCGTCTTCGGCGTGCCGGGCCACGTACACACCT
          P D P G A G S V E Q K P H G P V H V W T

      CAGGTGATCGCAACCAAGCCCAATCGCGAAGACATGGGCACGCTCTACTCGGCGCGTGCGG
481-----+-----+-----+-----+-----+-----+-----+-----+540
      GTCCACTAGCGTTGGTCGGGTTAGCGCTTCTGTACCCGTCGGAGATGAGCCGCCGACCC
          G D R N Q P N R E D M G T L Y S A A W D

      ACCCGGTTTTTTTCGCACACCAACGCAACATCGACCGCATGTGGTACGTGTGAGGAACC
541-----+-----+-----+-----+-----+-----+-----+-----+600
      TGGGGCAAAAAGCGTGTGGTGGCCGTTGTAGTGGCGGTACACCATGCACACCTCCTTGG
          P V F F A H H G N I D R M W Y V W R N L

```

FIGURE 8C

601-----+-----+-----+-----+-----+-----+660
TTGGGGCAAGCACC GCAACTTCACCGACCCCGACTGGCTCAACGCGTCCCTTCCCTGTTCT
AACCGCCGTTCTGGCGTTGAAGTGGCTGGGGCTGACCGAGTTGCCGAGGACGACAAGA
G G K H R N F T D P D W L N A S F L F Y
ACGACGAAAA
661-----+ 670
TGCTGCTTTT
D E

FIGURE 9A

```

1  TTGCCGTTTGGAAATGGGACGCCCGGGGGCATGCAGATCCCGGCCATCTACGCCGAC
   +-----+-----+-----+-----+-----+-----+-----+
61 AACGGCAAAACCTTAACCCCTGCGCGCCCCCGTACGTCTAGGGCCGGTAGATGCGGGCTG
   L P F W N W D A P G G M Q I P A I Y A D
   GCTTCGTCCCCGCTCTACGACAAGCTGCGCAATGCGAAGCACCAGCCCGGACCTTGGTC
   +-----+-----+-----+-----+-----+-----+-----+
121 CGAAGCAGGGCGGAGATGCTGTTTCGACGCCGTTACGCTTCGTGTCGGCGGCTGAAACCCAG
   A S S P L Y D K L R N A K H Q P P T L V
   GACCTCGACTACAACGGCACCGACCCGACCTTCACCCCTGAGCAGCAGATCGCCCAAC
   +-----+-----+-----+-----+-----+-----+-----+
181 CTGAGCTGATGTTGCCGTGGCTGGCTGGAAGTGGGACTCGTCGTCTAGCGGGTGTG
   D L D Y N G T D P T F T P E Q Q I A H N
   CTCACCATCATGTACCGACAGGTGATATCCGGCGGGAAGACGCCGGAGTTGTTATGGGC
   +-----+-----+-----+-----+-----+-----+-----+
241 GAGTGGTAGTACATGGCTGTCCACTATAGGCCCGCCCTTCTCGGGCCTCAACAAATACCCG
   L T I M Y R Q V I S G G K T P E L F M G
   GCGGCGTACCGCGGGGACGCGCCAGACCCGGCGCAGGCACTCTAGAGCTCGTGCCG
   +-----+-----+-----+-----+-----+-----+-----+
301 CGCCGCGATGGCGCGCCCGCTGCGCGGTCTGGGCCCCGCTCCGTGAGATCTCGAGCACGGC
   A A Y R A G D A P D P G A G T L E L V P

```

FIGURE 9B

CACAACACGATGCAATTGTGGACCGGCGACCCCAACCAACCGAAGACATGGGC
 301-----+-----+-----+-----+-----+-----+-----+360
 GTGTTGTGCTACGTAACACACCTGGCCGCTGGGGTTGGTTGGTTGCTGCTTCTGTACCCG
 H N T M H L W T G D P N Q P N D E D M G

 ACGTTCTACGGCGGCGGCGGACCCCATCTTCTCGCCCCACCGGCAACGTCGACCGC
 361-----+-----+-----+-----+-----+-----+-----+420
 TGCAAGATGCGCGCGCCCTGGGGTAGAAGACGGGTGGTGCCGTTGCAGCTGGCG
 T F Y A A A R D P I F F A H H G N V D R

 ATGTGTACGTGTGGCGGAAACTCGGGGCGACGCCGCGATTTCACCGACCCCGACTGG
 421-----+-----+-----+-----+-----+-----+-----+480
 TACACCATGCACACCGCCTTTGAGCCCCCGTGCGTGCGCTAAAGTGGCTGGGGCTGACC
 M W Y V W R K L G G T H R D F T D P D W

 CTCAACGCGTCCTTCTTCTACGACGAGAACGCGCAGCTCGTCCGCGTCAAAGTAAAG
 481-----+-----+-----+-----+-----+-----+-----+540
 GAGTTGCGCAGGAAGAGAAGATGCTGCTCTTGCGCGTTCGAGCAGCGCAGTTTCATTTC
 L N A S F L F Y D E N A Q L V R V K V K

 GACTGCTTGAGCGCGGACGCGCTGCGGTACACGTACCAGGACGTCGACATCCCGTGATC
 541-----+-----+-----+-----+-----+-----+-----+600
 CTGACGAACTCGCGGCTGCGCGACGCCCATGTGCATGGTCCCTGCAGCTGTAGGGCACCTAG
 D C L S A D A L R Y T Y Q D V D I P W I

FIGURE 9C

```

AGTGCAGAGCCGACGCCGGAAGAAACACCGGGGGCGCTGCGCCTTCCACGACAGAGGCT
601-----+-----+-----+-----+-----+-----+-----+660
TCACGCTTCGGCTGCGGCTTCCTTTGTGGCCCCCGCGACGCGGAAGGTGCTGTCTCCGA
S A K P T P K K T P G G A A P S T T E A

ATATTCCGGTGGTGGATAAGCCGGTGAGCTCTACGGTGGCGAGGCCGAAGACGGGG
661-----+-----+-----+-----+-----+-----+-----+720
TATAAGGCCACGACCTATTTCGGCCACTCGAGATGCCACCGCTCCGGCTTCTGCCCC
I F P V V L D K P V S S T V A R P K T G

AGGAGTACTGGGGAGGAGGAGGTGTTGGTGGAGGGAATCGAGCTGGACAAGGACGTG
721-----+-----+-----+-----+-----+-----+-----+780
TCCTCATGACCCCTCCTCCACAACCACCACCTCCCTTAGCTCGACCTGTTCCCTGCAC
R S T G E E V L V V E G I E L D K D V

GCCGTGAAGTTCGACGTGTATATAACGCGCCGACAAAGGGTGGGCGCGGAGGCG
781-----+-----+-----+-----+-----+-----+-----+840
CGGCACTTCAAGCTGCACATATATTGCGGGCCTGTGTCTTCCCCACCCCGCCTCCGC
A V K F D V Y I N A P D N E G V G P E A

AGCGAGTTCGAGGAGCTTCGTCCAGGTCCCGCACAAAGCAAGGGGAAGAAGGAG
841-----+-----+-----+-----+-----+-----+-----+900
TCGCTCAAGCTCCCTCGAAGCAGGTCCACGGCGTGTTCGTGTCTTCCCCTTCTCCTC
S E F A G S F V Q V P H K H K K G K K E

```


FIGURE 9D

```
901-----+-----+-----+-----+-----+-----+-----+-----+960
AAGCGAGGATTAAACGACGCTCAGGCTCGGATAACGGACCTGCTCGAGGACATCGGC
TTCCGCTCCTAATTTGCTGCGAGTCCGAGCCCTATTGCCCTGGACGAGCTCCTGTAGCCG
K A R I K T T L R L G I T D L L E D I G

961-----+-----+-----+-----+-----+-----+-----+-----+1020
GCCGAGGACGACGAGCGTGCTCGTCACGCTCGTGCCGAGGATAGGCCGAGGGTTGGTC
CGGCTCCTGCTGCTCTCGCACGAGCAGTGCGGAGCACGGCTCCTATCCGCTCCCCAACCCAG
A E D D E S V L V T L V P R I G E G L V

1021-----+-----+-----+-----+-----+-----+-----+-----+1080
AAGTTGGTGGGCTAAGGATCGATTCTCCAAGTGATCAGCAGCAATTAACATACATG
TTCCAACCACCCGATTCCCTAGCTAAGAGGTTCACTAGTCGTCGTTAATTGATATGTAC
K V G G L R I D F S K * S A A N * L Y M

1081-----+-----+-----+-----+-----+-----+-----+-----+1140
AAAGTAAAAAAATTGCATTTACCTACCTACCTATAGAAGAGAATAAATGCGTATGTAATCTGC
TTTCATTTTAAACGTAAATGGATGGATATCTCTCTTATTACGCATACATTAGACG
K V K K I A F T Y L * K R I N A Y V I C

1141-----+-----+-----+-----+-----+-----+-----+-----+1200
CCCATTTGTCACTTTAATTTCTCGAGCGTGTTCTGAATGAGAGTTGCATGCATGCGCGC
GGGTAAACAGTGAAAAATTAAAGAGCTCGCACAAAGACTTACTCTCAACGTACGTACGCGCG
P I C H F * F L E R V L N E S C M H A R
```

FIGURE 9E

```
AGCCATAATGCCCTGGTATAGTGTAGTAGTTTAGGCGTGGATACGTATAACGTACGTATGC
1201-----+-----+-----+-----+-----+-----+-----+1260
TCGGTATTACGGACCATATCACATCATCAAAATCCGCACCTATGCATATTGCATGCATACG
S H N A W Y S V V V * A W I R I T Y V C
ATGTATAAGGAATAATGATGAGTTTACTATGCAAAAAAAAAAAAAAAAAAAAA
1261-----+-----+-----+-----+-----+-----+-----1319
TACATATTCCTTATTACTACTCAAAATGATACGTTTTTTTTTTTTTTTTTTTTTTT
M Y K E * * * V Y Y A K K K K K K K K K
```

FIGURE 10A

1-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+60
 CGGTATCGATAAGCTTGATCCAGTGCCTGGTTAGTGTTACTATGCCCACCTCTC
 GCCATAGCTATTCGAACTAGGTCACGGACCAAATCCACATAAGTGATACCGGTGGAGAG
 G I D K L D P V P G L G V F T M A T L S

 61-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+120
 TAAACTAGCTTCCCAACCAATAACACCTCCACTCTCCCCGCTCCCTCTTGCATGCTCC
 ATTTGATCGAAGGTTGGTTATTGTGAGGTGAGAGGGCGGAGGAGGAAACGTACGAGG
 K L A S Q P I T P P L S P L P L H A P

 121-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+180
 TTCTCTACCAAAGCTTCACCAACCACTTCTCTCTCCCTGTAGGGTCCCCAAACCACCC
 AAGAGAGTGGTTTTCGAAGTGGTGGAGGAGAGGGACATCCCCAGGGTTTGGTGGG
 S L T K S F T T T F L S P V G V P N H P

 181-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+240
 CGTCATAAGATCTCATGCAAATCTAAGGAGCAACAAGAGAATGCCGACAAAGCCTGCGGGC
 GCAGTATCTAGAGTACGTTTAGATTCTCTCGTTGTTCTCTTACGGCTGTTCCGACGCCCG
 V I R S H A N L R S N K R M P T S L R A

 241-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+300
 CGCATCGCCCCGGACCTACTCTGGGCCCCCTCGGGGGCTTTACGGTGCCACCACTGG
 GCGTAGGGGGCGCTGGATGAGGACCCGGGAGCCGCCGAAATGCCACGGTGTGACC
 A S P A A T Y S W A L G G L Y G A T T G

FIGURE 10B

```
GCTCGGCCTCAACCGTCGAGGGCGCGCCCTATCCTGGCTCCCGACCTCTCAACTTG
301-----+-----+-----+-----+-----+-----+-----+360
CGAGCCGGAGTTGGCAGCTCGCCCGCGGGGGGATAGGACCGAGGGCTGGAGAGTTGAAC
    L G L N R R A A A A P I L A P D L S T C
TGGGCGGCCTGCCGACCTCCCTGCCCTCCGCCCGACCGACAGTTTGCTGCCCGCCATACCA
361-----+-----+-----+-----+-----+-----+-----+420
ACCCGGCGGACGGCTGGAGGACGGAGCGGGGCTGGCTGTCAAACGACGGCGGTATGGT
    G P P A D L P A S A R P T V C C P P Y Q
ATCCACCATCATCGACTTCAAGCTCCCCCGCATCTGCTCCGCTTCGCGTCCGGCCTGC
421-----+-----+-----+-----+-----+-----+-----+480
TAGGTGGTAGCTGAAGTTCGAGGGGGCGCTAGACGAGCGGAAGCGCAGCCGGACG
    S T I I D F K L P P R S A P L R V R P A
GGCCCACTTGTTGACGCCGACTACCTGGCCAAGTATAAGAAGCGGTCGAGCTCATGAG
481-----+-----+-----+-----+-----+-----+-----+540
CCGGTGAACCAACTGCGGCTGATGGACCGGTTTCATATTCTCCGCCAGCTCGAGTACTC
    A H L V D A D Y L A K Y K K A V E L M R
GGCCCTGCCGCGACGACCGGCAACTTCGTACAGCAAGCGAAAGTGCACGTGCGGTA
541-----+-----+-----+-----+-----+-----+-----+600
CCGGACGGCGGCTGCTGGGCGGTTGAAGCATGTCGTTTCGCTTTCACGTGACACGCAT
    A L P A D D P R N F V Q Q A K V H C A Y
```

FIGURE 10C

```

601-----+-----+-----+-----+-----+-----+-----+-----+660
      TTGCGACGGCGGTATGACCAAAATCGGCTTCCCGATCTCGAGATCCAGATCCACAACATC
      AACGCTGCCGCGCATACTGGTTTAGCCGAAGGGCTAGAGCTCTAGGTCTAGGTGTTGAG
          C D G A Y D Q I G F P D L E I Q I H N S
      GTGGCTCTTCTTCCCTTGGCACCGGTTCTACCTCTACTCCAACGAGCGCATACTCGGGAA
661-----+-----+-----+-----+-----+-----+-----+-----+720
      CACCGAGAAAGAAAGAACCGTGGCCAAAGATGGAGATGAGGTGCTCGCGTATGAGCCCTT
          W L F F P W H R F Y L Y S N E R I L G K
      ACTTATCGGGCAGACACGTTTCGGCTGCCCTTCTTGAACTGGGACGCCGGGGGGCAT
721-----+-----+-----+-----+-----+-----+-----+-----+780
      TGAATAGCCGCTGCTGTGCAAGCGCGACGGAAGACCTTGACCCCTGCGCGGCCCCCGTA
          L I G D D T F A L P F W N W D A P G G M
      GCAGTTCCCGTCTATCTACACAGACCCTTCATCCTCGCTATATGACAAGCTGCCGTGATGC
781-----+-----+-----+-----+-----+-----+-----+-----+840
      CGTCAAGGGCAGATAGATGTGCTGGGAAGTAGGAGCGGATATACTGTTTCGACGCACACG
          Q F P S I Y T D P S S S L Y D K L R D A
      GAAGCACCAGCCGCCGACTTTGATTGACCTCGACTACAATGGCACCAGTCCCTACCTCTC
841-----+-----+-----+-----+-----+-----+-----+-----+900
      CTTCTGCTCGGCGGCTGAAACTAACTGGAGCTGATGTTACCGTGGCTAGGATGGAAGAG
          K H Q P P T L I D L D Y N G T D P T F S

```

FIGURE 10D

CCCTGAAGAACAGATTAAACCACAACCTCGCCGTCATGTACCGACAGGTGATATCCAGTGG
901-----+-----+-----+-----+-----+-----+-----+960
GGGACTTCTTGTCTAATTGGTGTGGAGCGGCAGTACATGGCTGTCCACTATAGGTCACC
P E E Q I N H N L A V M Y R Q V I S S G
AAAGACGCCAGAGCTGTTTATGGGCTCAGCGTACCGCGCCGGTGACCGCCTGACCCCCGG
961-----+-----+-----+-----+-----+-----+-----+1020
TTTCTCGGTCTCGACAAATACCCGAGTCGCGATGGCGCGGCCACTGGTCGGACTGGGGCC
K T P E L F M G S A Y R A G D Q P D P G
CGCAGGCTCTGTAGAGCAGAAGCCGCACGCGCCCGGTGCAATGTGTGACAGGTGATCGCAA
1021-----+-----+-----+-----+-----+-----+-----+1080
GCGTCCGAGACATCTCGTCTTTCGGCGTGCCGGGCCACGTACACACCTGTCCACTAGCGTT
A G S V E Q K P H G P V H V W T G D R N
CCAGCCCCAATCGCGAAGACATGGGCACGCTCTACTCGCGCGGTGGACCCCGTCTTCTT
1081-----+-----+-----+-----+-----+-----+-----+1140
GGTCGGGTTAGCGCTTCTGTACCCGTGCGAGATGAGCCCGCCGACCCCTGGGCGAGAAGAA
Q P N R E D M G T L Y S A A W D P V F F
CGCACACCACGGCAACATCGACCGCATGTGGTACGTGTGGAGGAACCTTGGCGGCAAGCA
1141-----+-----+-----+-----+-----+-----+-----+1200
GCGTGTGGTGCCGTTGTAGCTGGCGGTACACCATGCACACCTCCTTGGAAACCGCCGTTTCGT
A H H G N I D R M W Y V W R N L G G K H

FIGURE 10E

```
1201-----+-----+-----+-----+-----+-----+1260
      CCGCAACTTCACCGACCCCGACTGGCTCAACGCGCTCCTTCCTGTTCTATGATGAGAAATGC
      GCGGTTGAAGTGGCTGGGCTGACCGAGTTGCGCAGGAAGGACAAGATACTACTCTTACG
      R N F T D P D W L N A S F L F Y D E N A

1261-----+-----+-----+-----+-----+-----+1320
      GCAGCTCGTCCGTGTTAAAGTAAAGACTGCTTAGAGGGCCGACGCAATGCGGTACACATA
      CGTCGAGCAGGCACAATTTTCATTCTTGACGAATCTCCGGCTGCGTTACGCCATGTGTAT
      Q L V R V K V K D C L E A D A M R Y T Y

1321-----+-----+-----+-----+-----+-----+1380
      CCAGGATGTAGAGATCCCCTGGCTCAAAGCAAAGCCGACGCCAAAGAGCGCCCTACAGAA
      GGTCTACATCTAGGGCACCGAGTTTCGTTTCGGCTGCGGTTTCTCGCGGATGTCTT
      Q D V E I P W L K A K P T P K S A L Q K

1381-----+-----+-----+-----+-----+-----+1440
      GATAAAGAGCAAGGTATCGACGCTGAAGGCAACACCAAGGGGACGACGACTACACAGC
      CTATTTCTCGTTCCATAGCTGCGACTTCCGTTGTGGTTCCCCCTGCTGCTGATGGTCTG
      I K S K V S T L K A T P R G T T T T A

1441-----+-----+-----+-----+-----+-----+1500
      AGAGACTACATTTCCGGTGTGTGGATAAGCCGGTGAGTGCAACAGTGGCTAGACCGAA
      TCTCTGATGTAAAGGCCACCGACCTATTTCGGCCACTCACGTTGTACCCGATCTGGCTT
      E T T F P V V L D K P V S A T V A R P K
```

1501-----+-----+-----+-----+-----+-----+1560
GCCAGGAGGAGTGGGAAGGAGAAGGAAGAGAGGAGGAGGTGTGTTGGTGGAGGGAAT
CCGGTCCCTCCTCACCCTTCCCTCTTCTCTCTCTCTCTCCACAACCAACCACTCCCTTA
A R S G K E K E E E E E E V L V V E G I
CGAGTTGGAAGGACGTGTTGTTGTAAGTTGATGTGTATATAAACTCGCCGGAGCACGA
1561-----+-----+-----+-----+-----+-----+1620
GCTCAACCTCTTCTGCAACAAGCACTTCAAACCTACACATATATTGAGCGGCTCGTGCT
E L E K D V F V K F D V Y I N S P E H E
AGGGTGGGCGGAGGCGAGTGAGTTCGCAGGAGCTTCGTCCACGTGCCACACAAGCA
1621-----+-----+-----+-----+-----+-----+1680
TCCCCACCCCGGCTCCGCTCACTCAAGCGTCCCTCGAAGCAGGTGCACGGTGTGTTCTG
G V G P E A S E F A G S F V H V P H K H
CAAGAAGCGGAAGGGAAGGAGATGGCCAGGATGAACACAAGGCTTAAGCTCGGGAT
1681-----+-----+-----+-----+-----+-----+1740
GTTCTTCGGCTTCTCCCTTCTCTACCGGTCTACTTGTGTCCGAATTCGAGCCCTA
K K A K K G K E M A R M N T R L K L G I
AACGGACCTGCTCGAGGACATCGGCGCTGAGGACGACGAGAGCGTGTCTATCACGCTCGT
1741-----+-----+-----+-----+-----+-----+1800
TTGCCCTGGACGAGCTCCTGTAGCCGCGACTCCTGCTGCTCTCGCACGAGTAGTGCGAGCA
T D L L E D I G A E D D E S V L I T L V

FIGURE 10G

1801-----+-----+-----+-----+-----+-----+-----+1860
GCCCAGGAGCGGCAAGGGAATGGTGAAGGTTGGAGGGCTAAGGATTGATTTCTCCAAGTG
CGGGTCCCTCGCCGTTCCCTTACCACCTTCCAACCTCCCGATTCTTAATAAGAGGTTTCAC
P R S G K G M V K V G G L R I D F S K *
ATGAGCATATTGTGAAGAGAAAAATTGCAATTACCGCCCTATAGAATCGAAAAAATTGCGT
1861-----+-----+-----+-----+-----+-----+1920
TACTCGTATAACACTTCTCTTTTAAACGTAATGGCGGGATATCTTAGCTTTTAAACGCA
* A Y C E E K I C I Y R P I E S K N C V
ATATGTCCCATTTATGTTTTTTTATTCTTCAAGCGTATTCAAGATAAGAGTTGCGTGCA
1921-----+-----+-----+-----+-----+-----+1980
TATACAGGGTAATAACAAAAAATAAGAAAGTTCGCATAAGTCTTATTCTCAACGCACGT
Y V P L L F F L F F K R I Q N K S C V H
TGCACGCATGCAGCCATGTTGTTGTAGTCGATATGTGGGGTATGTTTGATCAGGGATAA
1981-----+-----+-----+-----+-----+-----+2040
ACGTGCGTACGTCGGTACAACAACATCAGCTATACACCCCATACAAACCTAGTCCCTATT
A R M Q P C C C S R Y V G Y V W I R D N
TGATGTGAACCTTGAATTAATTATACACTCTGAGAATAAATTAGAGAGTTTATTATGCA
2041-----+-----+-----+-----+-----+-----+2100
ACTACACTTGAAACTTAATTAATAATGTGAGACTCTTATTTAATCTCTCAATAATACGT
D V N F E L I I T L * E * I R E F I M Q

FIGURE 10H

AGTTGCTTGGTGAATAGATATTCAACATTGTTTCCTATACATCTTTTGTGAAGAAA
2101-----+-----+-----+-----+-----+-----+2160

TCAACGAACCATTTATCTATAAGTTGTAACAAGGATATGTAGAAAAAACCTTCTTT
V A W C N R Y S T L F P I H L F L E E K

AAAAAAAAAAAAATCGAT

2161-----+-----+-- 2181

TTTTTTTTTTTTTTAGCTA

K K K K K S

FIGURE 11A

CAGCCACCCCTTCTCTCTCTCTCTGTTACTGAACAGTAATAGACATGTCCCT
+-----+-----+-----+-----+-----+60
GTGGGTGGGAAGAGAGAGAGAGAGACCAGATGACTTGTCATTATCTGTACAGGA
T P P F S L S L S L V Y * T V I D M S L

GCTGTTGAACCTTAGCTTCAACCGGTGCTTCCCTCTGCATGCCTCCTCCAACGGAAAGGC
61-----+-----+-----+-----+-----+120
CGACAACCTTGAGATCGAAGTGGCCACGAGGAGACGTACGGAGGAGTTGCCCTTCCAG
L L N S S F T G A S S A C L L Q R E R S

CCGCCGCCGCCCTCCACGTCCCCTGGCGTGACATGCCGCCAGGCAGTAATGGTGACCG
121-----+-----+-----+-----+-----+180
GGCGCGCGCGGAGGTGCAGGACCGCACTGTACGGCGTCCCCTCATTTACCACTGGC
R R R R L H V P G V T C R Q G S N G D R

CAGAGATCGCGCCCCCAGCAGCAGTCGCCCGCGCTGCTGGATCGGCGCGACATGCTGTT
181-----+-----+-----+-----+-----+240
GTCTCTACGGCGGGGGTTCGTCTCAGCGGGCGGACGACCTAGCCGCGCTGTACGACAA
R D A A P Q Q Q S P P L L D R R D M L L

GGGTTAGGAGGCTTTACGGCGTGACCGCAGGACCCAAAGTTCTGGCGGCGCCGATAAT
241-----+-----+-----+-----+-----+300
CCCAAATCCTCCCGAAATGCCGCACTGGCGTCTGGTTCCAAGACCGCGCGCTATTA
G L G G L Y G V T A G P K V L A A P I M

FIGURE 11B

```

GCCGCCGGATCTGTCCAAGTGCTACCCCTGCCACCCGCACCTGCCCTCGACAACAAATGCTG
301-----+-----+-----+-----+-----+-----+-----+360
CGCGCGCCTAGACAGGTTACACGATGGGACGGTGGCGTGGACGGGAGCTGTTGTTTACGAC
P P D L S K. C Y P A T A P A L D N K C C
CCC GCCCTTACGACCCCGCGAGACGATCTCGGAGTACAGCTTCCCCTGCTACGCCCTCCG
361-----+-----+-----+-----+-----+-----+-----+420
GGCGGGAATGCTGGGGCCGCTCTGCTAGAGCCCTCATGTGGAAGGACGATGCGGGGAGGC
P P Y D P G E T I S E Y S F P A T P L R
GGTGGCGCGCGCCCATATCGTGAAGGACGATCAGGAGTATATGGACAAGTACAAGGA
421-----+-----+-----+-----+-----+-----+-----+480
CCACGCCGCGCGCGGTATAGCACTTCCTGCTAGTCCCTCATATACCTGTTTCCT
V R R P A H I V K D D Q E Y M D K Y K E
GGCAGTGAGGAGGATGAAGAATCTGCCGGCAGACCACCCTTGGAACCTACTACCAGCAGGC
481-----+-----+-----+-----+-----+-----+-----+540
CCGTCACTCCTCCTACTTCTTAGACGGCCGCTCTGGTGGAAACCTTGATGATGGTCGTCGG
A V R R M K N L P A D H P W N Y Y Q Q A
GAACATCCACTGCCAGTATTGCAACTACGCCCTACCACCAGCAAAATACCGACGACGTGCC
541-----+-----+-----+-----+-----+-----+-----+600
CTTGTAGGTGACGGTCATAACGTTGATCGGGATGGTGTGCTGTTTATGGCTGCTGCACGG
N I H C Q Y C N Y A Y H Q Q N T D D V P

```

FIGURE 11C

```

CATCCAGGTCACCTCAGCTGGATCTCTCCCATGGCACCGCTACTACCTCCACTTCTA
601-----+-----+-----+-----+-----+-----+-----+660
GTAGGTCAGGTGAAGTCGACCTAGAAGGAGGTACCGTGGCGATGATGGAGGTGAAGAT
    I Q V H F S W I F L P W H R Y Y L H F Y
CGAAAGGATCCTCGGCAAGCTCATCGACGACACCTTCACCATCCCATTCTGGAACGT
661-----+-----+-----+-----+-----+-----+-----+720
GCTTTCCTAGGAGCCGTTTCGAGTAGCTGCTGTGGAAGTGTAGGGTAAGACCTTGAC
    E R I L G K L I D D D T F T I P F W N W
GGACACCAAGGACGGGATGACGTTCCCGCCCATCTTCAGGATGCGGCATCCCCGCTGTA
721-----+-----+-----+-----+-----+-----+-----+780
CCTGTGGTTCCTGCCCTACTGCAAGGGCGGTAGAAGTCTACGCCGTAGGGCGGACAT
    D T K D G M T F P A I F Q D A A S P L Y
CGACCCGAGACGCGACCAACGCCACGTCAAGGACGGCAAGATCCTCGACCTCAAGTACGC
781-----+-----+-----+-----+-----+-----+-----+840
GCTGGGCTCTGGCTGTTGCGGTGCAGTTCCTGCCGTTCTAGGAGCTGGAGTTCATGCCG
    D P R R D Q R H V K D G K I L D L K Y A
CTACACCGAAACACTGCATCCGACAGCGAGATCATACGGGAGAACCTCTGCTTCATACA
841-----+-----+-----+-----+-----+-----+-----+900
GATGTGGCTTTGTGACGTAGGCTGTCGCTCTAGTATGCCCTCTTGGAGACGAAGTATGT
    Y T E N T A S D S E I I R E N L C F I Q

```

FIGURE 11D

```
GAAGACGTTCAAGCACAGCCTGTGCTGGCGGAACTGTTTCATGGGGGATCCCCGTGCGGCGC
901-----+-----+-----+-----+-----+-----+-----+960
CTTCTGCAAGTTCGTGTCGGACAGCGACCGCCTTGACAAGTACCCCTAGGGCACGCGCG
      K T F K H S L S L A E L F M G D P V R A
GGGGGAGAAGGAGATCCAGGAGGCTAATGGGCAGATGGAAGTCATCCACAATGCGGCGCA
961-----+-----+-----+-----+-----+-----+-----+1020
CCCCCTCTTCCTCTAGGTCCTCCGATTACCCGCTCTACCTTCAGTAGGTGTTACGCCGCGT
      G E K E I Q E A N G Q M E V I H N A A H
CATGTGGTCTGGAGAGCCGGACGGATACAAGGAAAACATGGGGGACTTCTCCACCGCCGC
1021-----+-----+-----+-----+-----+-----+-----+1080
GTACACCCAGCCTCTCGGCCTGCCCTATGTTCCCTTTGTACCCCTGAAGAGGTGGCGGCG
      M W V G E P D G Y K E N M G D F S T A A
CCGCGATTCTGTTTCTCTGCCACCATTCCTCAATGTCGACCGCATGTGGGACATCTACCG
1081-----+-----+-----+-----+-----+-----+-----+1140
GGCGCTAAGACAAAAGAAGACGGTGGTAAGGTTACAGCTGGCGTACACCCCTGTAGATGGC
      R D S V F F C H S N V D R M W D I Y R
CAACCTCCGGCAACCGCGTCGAGTTCGAAGACAACGACTGTTGGACAGCACCTTCCT
1141-----+-----+-----+-----+-----+-----+-----+1200
GTTGGAGCGCGGTTGGCGCAGCTCAAGCTTCTGTTGCTGACCAACCTGTCTGGAAGGA
      N L R G N R V E F E D N D W L D S T F L
```

FIGURE 11E

CTTCCACGAGAACGAACAGCTCGTCAAAAGTC AAGATGAGCGACTGCCCTCAACC GCAC
+-----+-----+-----+-----+-----+-----+
1201 +-----+-----+-----+-----+-----+-----+1260

GAAGGTGCTGCTCTTGCTTGTCGAGCAGTTTCAGTTC TACTCGCTGACGGAGTTGGGCTG
F H D E N E Q L V K V K M S D C L N P T
+-----+-----+-----+-----+-----+-----+

CAAGCTTCGGTACACGTTTCGAGCAAAGTTC CCCCTCCC ATGGCTGGCAAATAAATTGCCA
+-----+-----+-----+-----+-----+-----+
1261 +-----+-----+-----+-----+-----+-----+1320

GTT CGAAGCCATGTG CAAGCTCGTTCAAGGGGAGGT ACCGACCCGTTTTAGTT AACGGT
K L R Y T F E Q V P L P W L G K I N C Q
+-----+-----+-----+-----+-----+-----+

GAAGACGGCAGAGACGAAGTCCAAGGCCACG ACGGAGCTGTCGCTGACGC GCGTGAACGA
+-----+-----+-----+-----+-----+-----+
1321 +-----+-----+-----+-----+-----+-----+1380

CTTCTGCCGCTCTGCTTCAGGTTCCGGTGCTGCCTC GACAGCGACTGCGCGCACTTGCT
K T A E T K S K A T T E L S L T R V N E
+-----+-----+-----+-----+-----+-----+

ATTCGGACGACGGCCAGGCACTCGACGCGAGCA ACCCGCTGCGGGTGATCGTGGCAAG
+-----+-----+-----+-----+-----+-----+
1381 +-----+-----+-----+-----+-----+-----+1440

T AAGCCCTGCTGCCGGGTC CGTGAGCTGCGCTCG TTGGCGACGCCCACTAGCACCGTTC
F G T T A Q A L D A S N P L R V I V A R
+-----+-----+-----+-----+-----+-----+

GCCGAAGAAGAACCGCAAGAAAGGAGAAGCA AGAAGGTGGGGTGATTCA GATCAA
+-----+-----+-----+-----+-----+-----+
1441 +-----+-----+-----+-----+-----+-----+1500

C GGCTTCTTCTTGCGGTTCTTCTTCTCTTCTGTTCT CTTCACCCCCCACTAAGTCTAGTT
P K K N R K K K E K Q E K V G V I Q I K
+-----+-----+-----+-----+-----+-----+

FIGURE 11F

```
1501-----+-----+-----+-----+-----+-----+-----+1560
      GGATATTAAAGTGACCAACGAGACAGCTCGCTTCGACGTCTATGTGCGGTTCCCTTA
      CCTATAATTCCACTGGTGGTTGCTCTGTGCGAGCGAAGCTGCAGATACAGCGCCAAGGAAT
          D I K V T T N E T A R F D V Y V A V P Y

1561-----+-----+-----+-----+-----+-----+-----+1620
      CGGTGACCTCGCCGACCCGACTACGGCGAGTTGCGGGCAGCTACGTGAGGCTGGCGCA
      GCCACTGGAGCGGCCTGGGCTGATGCCGCTCAAGCGCCCGTCGATGCACTCCGACCGCGT
          G D L A G P D Y G E F A G S Y V R L A H

1621-----+-----+-----+-----+-----+-----+-----+1680
      TAGGATGAAGGAAGCGACGGGACCGAAAGCAGGGCCCCAAGAAGGAAACTCAA
      ATCCTACTTCCCTTCGCTGCCCTGGCTTTTCGTCCCGGGGTTCTTCTCCCTTTGAGTT
          R M K G S D G T E K Q G P K K K G K L K

1681-----+-----+-----+-----+-----+-----+-----+1740
      GCTGGGTATTACGCCGCTGCTCGAGGACATCGATGCTGAGGACGCCGACAAGTTGGTGGT
      CGACCCATAATGCGGCGACGAGCTCCTGTAGCTACGACTCCTGCGGCTGTTCACACCACCA
          L G I T P L L E D I D A E D A D K L V V

1741-----+-----+-----+-----+-----+-----+-----+1800
      CACCCTGGTTCTCCGCACTGGGAGCGTCACCGTGGGGGGAGTTTCCCATCAATCTCCTGCA
      GTGGACCAAGAGGCGTGACCCCTCGCAGTGGCACCCCCCTCAAGGTAGTTAGAGGACGT
          T L V L R T G S V T V G G V S I N L L Q
```


FIGURE 11G

1801-----+-----+-----+-----+-----+-----+-----+1860
GACAGATTCTACCGCGCCATCTAAATGATGGCCTCGGATCACAGCTTCTCCCGCTTAA
CTGTCTAAGATGGCGGGTAGATTTTACTACCGGAGCCCTAGTGTCTGAAGAGGGGCGGAATT
T D S T A A I *
1861-----+-----+-----+-----+-----+-----+-----+1920
GTTGGAGTGATCGATTACTGGTGTCTTCTTCTCCTCCCTGTCGTTCTTGCTATCTTCTT
CAACCTCACTAGCTAATGACCACGACGAGAAAGAGGGACAGCAAGAACGATAGAAAGAA
1921-----+-----+-----+-----+-----+-----+-----+1980
GATCTGGAACGATCCCTTCAATAATTAGGGCATGACAGTAGTCGTCGCCCGATCCCATATG
CTAGACCTTGCTAGGAAGTTATTAATCCCGTACTGTCTATCAGCAGCGGGCTAGGGTATAC
1981-----+-----+-----+-----+-----+-----+-----+2040
TACGTGTTGGTCTCAACAGCTGTACATGTGACGTTATGGTGTGACTATATATTTTATTGC
ATGCACAACCAAGAGTTGTCGACATGTACACTGCAATACCACTGATATATAAAATAACG
2041-----+-----+-----+-----+-----+-----+-----+2078
GGTCATCCTTGTTTCTTTCTTAAATAAAAAAAAAA
CCAGTAGGAACAAGAAAGAAATTTTTTTTTTTTTTTT

FIGURE 12A

```

AATGTGGATCGGATGTGGACGGTGTGGAAGCTGCACGGCGACAAAGCCGGAGTTCGTC
1-----+-----+-----+-----+-----+-----+-----+60
TTACACCTAGCCTACACCTGCCACACCTTCTTCGACGTGCCGCTGTTCGGCCTCAAGCAG
  N V D R M W T V W K K L H G D K P E F V

GACCAGGAGTGGCTCGAGTCTGAATTACACCTTCTACGACGAGAATGTGCGCCTGCGCAGG
61-----+-----+-----+-----+-----+-----+-----+120
CTGGTCCCTACCCGAGCTCAGACTTAAAGTGGAAGATGCTGCTCTTACACGCGGACGCGTCC
  D Q E W L E S E F T F Y D E N V R L R R

ATCAAGGTGCGCGACGTGTTGAACATAGACAAACTCAGGTACCGGTACGAAGACATCGAC
121-----+-----+-----+-----+-----+-----+-----+180
TAGTTCCACGCGCTGCACAACTTGATCTGTGTTGAGTCCCATGGCCATGCTTCTGTAGCTG
  I K V R D V L N I D K L R Y R Y E D I D

ATGCCATGGCTCGCTGCACGTCCCAAGCCTTCCGTTCAACCCCTAAGATCGCGCGGACATA
181-----+-----+-----+-----+-----+-----+-----+240
TACGGTACCGAGCGACGTGCAGGGTTCGGAAGGCAAGTGGGATTCTAGCGCGCGCTGTAT
  M P W L A A R P K P S V H P K I A R D I

TTGAAGAAGCGTAATGGCGAAGCGGTACTGAGAATGCCCGCGGAAACGGATCGTTCACAA
241-----+-----+-----+-----+-----+-----+-----+300
AACTTCTTCGCATTACCGCTTCCGCATGACTCTTACGGGGCCGCTTTCCTAGCAAGTGT
  L K K R N G E G V L R M P G E T D R S Q

```

FIGURE 12B

```
CTCTCCGAAGATGGTAGCTGGACACTGGACAAAGAGCATCACCGTGAGGGTTGACAGGCCA
301-----+-----+-----+-----+-----+-----+-----+360
GAGAGGCTTCTACCATCGACCTGTGACCTGTTCTCGTAGTGGCACTCCCAACTGTCCGGT
L S E D G S W T L D K S I T V R V D R P

AGGATCAACAGGACAGGGCAAGAAAAGAGGAAGAGAGAGATCTTATTGGTCTACGGA
361-----+-----+-----+-----+-----+-----+-----+420
TCCTAGTTGTCCCTGTCCCGTTCTTTTCTCCTTCTCTCCTCTAGAATAACCATGTCCT
R I N R T G Q E K E E E E I L L V Y G

ATCGATACTAAGAGAAGCAGATTTCGTCAAATTCGATGTGTTTCATCAACGTCGTCGACGAA
421-----+-----+-----+-----+-----+-----+-----+480
TAGCTATGATTCTCTTCGTCTAAGCAGTTTAAAGCTACACAAGTAGTTGCAGCAGCTGCTT
I D T K R S R F V K F D V F I N V V D E

ACCGTGCTGAACCCAAAGTCGAGGGAGTTCGCAGGGACCTTCGTCAATCTCCACCACGTC
481-----+-----+-----+-----+-----+-----+-----+540
TGGCAGCACTTGGGTTTCAGCTCCCTCAAGCGTCCCTGGAAGCAGTTAGAGGTGGTGCAG
T V L N P K S R E F A G T F V N L H H V

TCGAGGACGAAAAGCCATGAGGATGGCGGGGTGGTTCGAAGATGAAAAGCCACCTTAAG
541-----+-----+-----+-----+-----+-----+-----+600
AGCTCCTGCTTTTCGGTACTCTACCGCCGCAACCAAGCTTCTACTTTTCGGTGGAAATC
S R T K S H E D G G V G S K M K S H L K
```

FIGURE 12C

```

CTCGGTATATCGGAACCTTTTGAAGACCTCGAGGCAGACGAAGATGATTGCATCTGGGTG
601-----+-----+-----+-----+-----+-----+-----+660
GAGCCATATAGCCTTGAAAACCTTCTGGAGCTCCGCTCTGCTTCTACTAACGTAGACCCAC
  L  G  I  S  E  L  E  L  E  D  L  E  A  D  E  D  D  C  I  W  V
ACACTGGTGCCAAGAGGGCGCACGGGGGTCAACACCACCGTAGACGGCGTCCGGATCGAC
661-----+-----+-----+-----+-----+-----+-----+720
TGTGACCACGGTTCTCCGCCGTGCCCCAGTTGTGTGGCATCTGCCGCGAGGCCTAGCTG
  T  L  V  P  R  G  G  T  G  V  N  T  T  V  D  G  V  R  I  D
TACATGAAGTAGTGAACCGGCACGCCGCTCCTCCCCATCAGAAAGTGGTATAATAT
721-----+-----+-----+-----+-----+-----+-----+780
ATGTACTTCATCACTTGGCCGTGCGGCGAGGAGGGGGTAGTCTTCACCATAATTATA
  Y  M  K  *
TTATATTGGATCGAGGCTCGTGGTATCTTTTGATAAGAGTAAGTCCATAAATTTAGAAG
781-----+-----+-----+-----+-----+-----+-----+840
AATATAACCTAGCTCCGAGCACCATAGAAAACATATTCTCATTTCAAGGTATTTAAATCTTC
AAGAATCATGTTCTTTATTATTATAATCAATCAATGTGATTGTCCAAAAAATAAAAAA
841-----+-----+-----+-----+-----+-----+-----+900
TTCTTAGTACAAGAAATAAATAATTAGTTACACTAAACAGGTTTTTTTTTTTTTTTT

```

FIGURE 13A

```

1-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+60
TGCACGTGTCGTATTGCGACGGCGCGTATGACCAAATCGGCTTCCCCGATCTCGAGATCC
ACGTGACACGCATAACGCTGCCGCGCATACTGGTTAGCCGAAGGGCTAGAGCTCTAGG
    H C A Y C D G A Y D Q I G F P D L E I Q
61-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+120
AGATCCACAACTCGTGGCTCTTCTTCCCTTGGCACCGGTTCTACCTCTACTCCAACGAGC
TCTAGGTGTTGAGCACCGAGAAAGAAAGAACCGTGGCCCAAGATGGAGATGAGGTTGCTCG
    I H N S W L F F P W H R F Y L Y S N E R
121-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+180
GCATACTCGGAAACTTATCGGCGACGACACGTTCCGCGTGCCTTCTGGAAC TGGGACG
CGTATGAGCCCTTTGAATAGCCGCTGCTGTGCAAGCGCGACGGAAGACCTTGACCC TGC
    I L G K L I G D D T F A L P F W N W D A
181-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+240
CGCCGGGGCATGCAGTTCCTGCTATCTACACGACCCCTTCATCCTCGCTATATGACA
GGGCCCCCGTACGTCAAGGGCAGATAGATGTGCTGGGAAGTAGGAGCGATATACTGT
    P G G M Q F P S I Y T D P S S S L Y D K
241-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+300
AGCTGCGTGATGCGAAGCACCGCCGCGACTTGTGATTGACCTCGACTACAATGGCACCG
TCGACGCACTACGCTTCGTGGTCGGCGGCTGAAACTAACTGGAGCTGATGTTACCGTGCG
    L R D A K H Q P P T L I D L D Y N G T D

```

FIGURE 13B

```

ATCCTACCTTCTCCCTGAAGAACAGATTAAACCACAACCTCGCCGTCATGTACCGACAGG
301-----+-----+-----+-----+-----+-----+-----+360
TAGGATGGAAGAGGGGACTTCTTGCTAATTGGTGTGGAGCGGCAGTACATGGCTGTCC
    P T F S P E E Q I N H N L A V M Y R Q V

TGATATCCAGTGGAAGACACCAGAGCTGTTTATGGGCTCAGCGTACCGCGCCGGTGACC
361-----+-----+-----+-----+-----+-----+-----+420
ACTATAGGTCACCTTCTGTGGTCTCGACAAATACCCGAGTCGCGATGGCGGCCACTGG
    I S S G K T P E L F M G S A Y R A G D Q

AGCCTGACCCCGCGCAGGCTCTGTAGAGCAGAAGCCGACGGCCCGGTGCATGTGTGGA
421-----+-----+-----+-----+-----+-----+-----+480
TCGGACTGGGCGCGTCCGAGACATCTCGTCTTCGGCGTGCCGGGCCACGTACACACCT
    P D P G A G S V E Q K P H G P V H V W T

CAGGTGATCGCAACCAGCCCAATCGCGAAGACATGGGCACGCTCTACTCGGCGCGGTGGG
481-----+-----+-----+-----+-----+-----+-----+540
GTCCACTAGCGTTGGTCGGGTTAGCGCTTCTGTACCCGTGCGAGATGAGCCGCCGACCC
    G D R N Q P N R E D M G T L Y S A A W D

ACCCCGTCTTCTTCGCACACCACGGCAACATCGACCGCATGTGGTACGTGTGGAGGAACC
541-----+-----+-----+-----+-----+-----+-----+600
TGGGGCAGAAGCGTGTGGTGCCGTTGTAGCTGGCGGTACACCATGCACACCTCCTTGG
    P V F F A H H G N I D R M W Y V W R N L

```

FIGURE 13C

```

601-----+-----+-----+-----+-----+-----+-----+-----+660
      TTGGCGCAAGCACCGCAACTTCACCGACCCCGACTGGCTCAACGCGTCCTTCCTGTTCT
      AACCGCCGTTTCGTGGCGTTGAAGTGGCTGGGGCTGACCGAGTTGCGCAGGAAGGACAAAGA
            G G K H R N F T D P D W L N A S F L F Y
661-----+-----+-----+-----+-----+-----+-----+-----+720
      ATGATGAGAAATGCGCAGCTCGTCCGTGTTAAAGTAAAGACTGCTTAGAGGCCGACGCAA
      TACTACTCTTACGCGTCGAGCAGGCACAAATTTTCATTTTCTGACGAAATCTCCGGCTGCGTT
            D E N A Q L V R V K V K D C L E A D A M
721-----+-----+-----+-----+-----+-----+-----+-----+780
      TCGGGTACACATACCAGGATGTAGAGATCCCGTGGCTCAAAGCAAAGCCGACGCCAAAGA
      ACGCCATGTGTATGGTCCCTACATCTCTAGGGCACCGAGTTTTCGTTTCGGCTGCGGTTTCT
            R Y T Y Q D V E I P W L K A K P T P K S
781-----+-----+-----+-----+-----+-----+-----+-----+840
      GCGCCCTACAGAAGATAAAGAGCAAGGTATCGACGCTGAAGGCAACACCAAGGGGACGA
      CGCGGGATGTCTTCTATTTCTCGTTCCATAGCTGCGACTTCCGTTGTGGTTCCCCCTGCT
            A L Q K I K S K V S T L K A T P R G T T
841-----+-----+-----+-----+-----+-----+-----+-----+900
      CGACTACCACAGCAGAGACTACATTTCCGGTGGTGTGATAGCCGGTGAGTGCAACAG
      GCTGATGGTGTCTCTGTATGTAAAGGCCACCGACCTATTCGGCCACTCACGTTGTC
            T T T A E T T F P V V L D K P V S A T V

```

TGGCTAGACCGAAGGCCAGGAGTGGGAAGGAGAAGAAAGAGGAGGTGTTGG
901-----+-----+-----+-----+-----+-----+960
ACCGATCTGGCTTCGGTCCCTCACCCCTCCTCCTCCTCCTCCTCCTCAACAACC
A R P K A R R S G K E K E E E E V L V

TGGTGGAGGGAATCGAGTTGGAGAAGGACGTTCGTGAAGTTTGATGTGTATATAAACT
961-----+-----+-----+-----+-----+-----+1020
ACCACCTCCCCTTAGCTCAACCTCTTCCTGCACAAGCACTTCAAACCTACACATATATTGA
V E G I E L E K D V F V K F D V Y I N S

CGCCGGAGCACGAAGGGTGGGGCCGGAGGCGAGTGAGTTCGCAGGGAGCTTCGTCCACG
1021-----+-----+-----+-----+-----+-----+1080
GCGGCTCGTGCTTCCCCACCCCGCCTCCGCTCACTCAAGCGTCCCTCGAAGCAGGTGC
P E H E G V G P E A S E F A G S F V H V

TGCCACACAAGCACAGAAGCGGAAGGAAGGAGATGCCAGGATGAACACAAGGC
1081-----+-----+-----+-----+-----+-----+1140
ACGGTGTGTTCTCGTCTTCCGCTTCTTCCCCTTCTCCTCTACCGTCTACTTGTGTCCG
P H K H K K A K K G K E M A R M N T R L

TTAAGCTCGGGATAACGGACCTGCTCGAGGACATCGGCGCTGAGGACGACGAGCGTGC
1141-----+-----+-----+-----+-----+-----+1200
AATTCGAGCCCTATTGCCTGGACGAGCTCCTGTAGCCGCGACTCCTGTCTCTCGCAGC
K L G I T D L L E D I G A E D D E S V L

FIGURE 13E

```

1201-----+-----+-----+-----+-----+-----+-----+-----+-----+1260
TCATCAGCGCTCGTGCCCGAGGAGCGGCAAGGGAATGGTGAAGGTTGGAGGGCTAAGGATTG
AGTAGTGGAGCACGGGTCCTCGCCGTTCCCTTACCACCTTCCAACCTCCCGATTCCCTAAC
  I T L V P R S G G K G M V K V G G L R I D

1261-----+-----+-----+-----+-----+-----+-----+-----+-----+1320
ATTTCTCCAAGTGATGAGCATAATTGTGAAGAGAGAAAATTTGCATTTACCGCCCTATAGAAT
TAAAGAGGTTCACTACTCGTATAACACTTCTCTTTTAAACGTAAATGGCGGGATATCTTA
  F S K * * A Y C E E K I C I Y R P I E S

1321-----+-----+-----+-----+-----+-----+-----+-----+-----+1380
CGAAAAAATTGCGGTATATGTCCCATTTATTGTTTTTTTTTTTATTCTTCAAGCGTATTCAGAATA
GCTTTTAAACGCATATACAGGGTAATAACAAAAAATAAGAGTTCCGCATAAGTCTTAT
  K N C V Y V P L L F F L F F K R I Q N K

1381-----+-----+-----+-----+-----+-----+-----+-----+-----+1440
AGAGTTGCGTGCGATGCACGCGATGCAGCCCATGTTGTTGTAGTCGATATGTGGGGTATGTTT
TCTCAACGCACGTACGTGCGTACGTGCGTACAAACAACATCAGCTATACACCCCATACAAA
  S C V H A R M Q P C C C S R Y V G Y V W

1441-----+-----+-----+-----+-----+-----+-----+-----+-----+1500
GGATCAGGGGATAATGATGTGAACCTTTGAATTAAATTATTACACTCTGAGAAATAATTAGAG
CCTAGTCCCTATTACTACACTTGAAACTTAATAATAATGTGAGACTCTTATTTAATCTC
  I R D N D V N F E L I I T L * E * I R E

AGTTTATTATGCAAAAAA
1501-----+-----+-----+-----+-----+-----+-----+-----+-----+1522
TCAAATAATACGTTTTTTTTT
  F I M Q K K

```

FIGURE 14A

```

ACAACAAACAGTGCCTGGTTTAGTGTATTCACTATGCCACCCCTCTCTAAACTAGCTT
1-----+-----+-----+-----+-----+-----+-----+60
TGTGTTTGGTCACGACCAATCCACATAAGTATACCGGTGGAGAGATTGATCGAA
      N K P V P G L G V F T M A T L S K L A S

CCCCAACCAATAACACCTCCACTCTCCCCGCTCCCTTTCATGCTCCTTCTCTCACC
61-----+-----+-----+-----+-----+-----+-----+120
GGGTTGGTTATTGTGAGGTGAGAGGGCGAGGAGGAAACGTACGAGGAAGAGAGTGG
      P T N N T S T L P A P S F A C S F S H Q

AAAAGCTTCACCACCACCTTCCTCTCTCCCTGTAGGGTCCCAACCCCGTCATAAGA
121-----+-----+-----+-----+-----+-----+-----+180
TTTTCGAAGTGGTGGTGAAGGAGAGGGGACATCCCCAGGTTTGGTGGGCGAGTATCT
      K L H H H L P L P C R G P K P P R H K I

TCTCATGCAAATCTAAGGAGCAACAAGAGAAATGCCGACAAAGCCTGCGGGCGCATCGACC
181-----+-----+-----+-----+-----+-----+-----+240
AGAGTACGTTTAGATTCTCCTCGTTGTTCTCTTACGGCTGTTCCGACGCCCCGGCGTAGCTGG
      S C K S K E Q Q E N A D K P A G R I D R

GCCGCGACCTACTCCTGGGCCCTCGCGGGGCTTTACGGTGCCACCACCTGGGCTCGGCCTCA
241-----+-----+-----+-----+-----+-----+-----+300
CGCGGCTGGATGAGACCCGAGCCGCCCGAAATGCCACGGTGTGACCCGAGCCGGAGT
      R D L L L G L G L Y G A T T G L G L N

```

FIGURE 14B

```

301-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+360
      ACCGTCGAGCGCGCGCCCTATCCTGGCTCCCGACCTCTCAACTTGTGGCGCGCCTG
      TGGCAGCTCGCCCGCGCGGGGATAGGACCGAGGGCTGGAGAGTTGAACACCCGCGGAC
      R R A A A A P I L A P D L S T C G P P A

361-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+420
      CCGACCTCCCTGCCTCCGCCCGACCGACAGTTTGCTGCCCGCATACCAATCCACCATCA
      GGCTGGAGGACGAGCGGGCTGGCTGTCAAACGACGGCGGTATGGTTAGGTGAGT
      D L P A S A R P T V C C P P Y Q S T I I

421-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+480
      TCGTCTTCAAGCTCCCCCGCATCTGCTCCGCTTCGGTCCGGCTGCGGCCACTTGG
      AGCAGAAAGTTCGAGGGGGCGCTAGACGAGGCGAAGCGCAGCCGACGCCGGTGAACC
      V F K L P P R S A P L R V R P A A H L V

481-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+540
      TTGACGCCGACTACCTGGCCAAGTATAAGAAGCGGTTCGAGCTCATGAGGCCCTGCCCGG
      AACTGCGGCTGATGGACCGGTTTCATATTCTTCCGCCAGCTCGAGTACTCCCGGACGGCC
      D A D Y L A K Y K K A V E L M R A L P A

541-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+600
      CCGACGACCCGCGCAACTTCGTACAGCAAGCGAAAGTGCACTGTGCGTACTGCGACGGCG
      GGCTGCTGGCGCGTTGAAGCATGTCGTTTCGCTTTCACGTGACACGCATGACGCTGCCGC
      D D P R N F V Q Q A K V H C A Y C D G A
  
```

FIGURE 14C

```

CGTACGACCAATCGGCTTCCCGATCTCGAGATCCAGATCCACAACCTCGTGGCTCTTCT
601-----+-----+-----+-----+-----+-----+660
GCATGCTGTTTAGCCGAAGGGCTAGAGCTCTAGGTCTAGGTGTGAGCACCGAGAAGA
    Y D Q I G F P D L E I Q I H N S W L F F
TTCCTTGGCACC GTTCTACCTCTACTTCAACGAGCGCATACTCGGGAACCTTATCGGTG
661-----+-----+-----+-----+-----+-----+720
AAGGAACCGTGGCCAAAGATGGAGATGAAGTTGCTCGCGTATGAGCCCTTTGAATAGCCAC
    P W H R F Y L Y F N E R I L G K L I G D
ACGACACGTTCCGGCTGCCCTTCTGGAACCTGGGACGCCGCGGGGGCATGCAGTTCCCGT
721-----+-----+-----+-----+-----+-----+780
TGCTGTGCAAGCGGACGGAAGACCTTGACCCCTGCGCGGCCCCCGTACGTCAAGGGCA
    D T F A L P F W N W D A P G G M Q F P S
CTATCTACACAGACCCTTCATCCTCGCTATATGACAAGCTGCGTGATGCCGAAGCACCAGC
781-----+-----+-----+-----+-----+-----+840
GATAGATGTGCTGGGAAGTAGGAGCGGATATACTGTTGACGCGCACTACGCTTCGTGGTGG
    I Y T D P S S S L Y D K L R D A K H Q P
CGCCGACTTTGATTGACCTCGACTACAATGGCACA
841-----+-----+-----+-----+-----+-----+875
GCGGCTGAAACTAACTGGAGCTGATGTTACCGTGT
    P T L I D L D Y N G T

```

FIGURE 15A

```

1-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+60
GACCACCCATAGATGAGCTTCTCTCGCCTTGTCTAGTCTTCCACCTCCACCACAACC
CTGGTGGGTATCTACTACCGAAGAGAGCGGAACAGATCAGAAGGGTGGAGGTGGTGTGG
      M A S L A L S S L P T S T T T
61-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+120
AAAAAACCCCTTATTTCCAAAACATCCTCGCATGTTAAGCCATTCCATCGCTTCAAAGTT
TTTTTTGGGAATAAAAGGTTTGTAGAGCGGTACAATTTCGGTAAGGTAGCGAAGTTTCAA
      K K P L F S K T S S H V K P F H R F K V
121-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+180
TCATGCAATGCACCCGCTGATAACAATGACAAAACCGTCAATAATTCTGATACCCCAAAG
AGTACGTTACGTGGCGGACTATTGTTACTGTTTGGCAGTTATTAAAGACTATGGGGTTTC
      S C N A P A D N N D K T V N N S D T P K
181-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+240
CTCATACTACCCAAACACCCACTTGAAACGCAGAACGTAGACAGGAGAAACTTGCTTCTG
GAGTATGATGGGTTTGTGGTGAACCTTTCGCTCTTTCATCTGTCCTCTTTGAACGAAGAC
      L I L P K T P L E T Q N V D R R N L L L
241-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+300
GGA CTCGGAGGTCTCTACGGCGCTGCCAACTTGACGACCATTCCGTCAGCCTTTGGCATT
CCTGAGCCTCCAGAGATGCCCGGACGGTTGAACTGCTGGTAAGGCAGTCGGAAACCGTAA
      G L G G L Y G A A N L T T I P S A F G I

```

FIGURE 15B

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301-----+-----+-----+-----+-----+-----+-----+360
      C C C A T C G C T C C A G A C A A T A T T C A G A C T G T G T T G C T G C G A C T T C A A A C C T A A G G A A C
      G G G T A G C G A C G A G G T C T G T T A T A A G T C T G A C A C A A C G A C G C T G A A G T T T G G A T T C C T T G
      P I A A P D N I S D C V A A T S N L R N

361-----+-----+-----+-----+-----+-----+-----+420
      A G C A A A G A C G C T A T A A G G G A C T A G C G T G T T G T T C C T C C G G T G C T T T C A A C A A A C A A A C C A
      T C G T T T C T G C G A T A T T C C C C T G A T C G C A C A A C A G G A G G C C A C G A A A G T T G T T G T T T G G T
      S K D A I R G L A C C P P V L S T N K P

421-----+-----+-----+-----+-----+-----+-----+480
      A T G G A T T A C G T C C T T C C A A C C C T G T G A T T C G T G T T C G A C C A G C T G C A C A G A A A G C C
      T A C C T A A T G C A G G A A G A G T T T G G A C A C T A A G C A C A A G C T G G T C G A C G T G T C T T T C G G
      M D Y V L P S N P V I R V R P A A Q K A

481-----+-----+-----+-----+-----+-----+-----+540
      A C T G C C G A T T A C A C T G C T A A G T A T C A A C A A G C A A T T C A A G C C A T G A A G G A T C T C C C C G A G
      T G A C G G C T A A T G T G A C G A T T C A T A G T T G T T C G T T A A G T T C G G T A C T T C C T A G A G G G G C T C
      T A D Y T A K Y Q Q A I Q A M K D L P E

541-----+-----+-----+-----+-----+-----+-----+600
      G A C C A C C A C A T A G C T G G A A G C A A C A A G G C A A G A T T C A C T G T G C T T A T T G C A A C G G T G G T
      C T G G T G G T G T A T C G A C C T T C G T T G T T C C G T T C T A A G T G A C A C A C G A A T A A C G T T G C C A C C A
      D H P H S W K Q Q Q G K I H C A Y C N G G

```

FIGURE 15C

```
601-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+660
TACAATCAAGAAACAAAGTGGTTACCCGAATTTACAACCTTCAGATTCACAACCTCATGGCTC
ATGTTAGTTCCTTGTTCACCAATGGGCTTAAATGTTGAAGTCTAAGTGTGAGTACCGAG
Y N Q E Q S G Y P N L Q L Q I H N S W L

661-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+720
TTCCTTTCCTTCCACCGGTGGTACCTCTATTTCTACGAGAAGATATTGGGGAAGTTGATT
AAGAAAGGAAAGGTGGCCACCATGGAGATAAAGATGCTCTTCTATAACCCCTTCAACTAA
F F P F H R W Y L Y F Y E K I L G K L I

721-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+780
AATGATCCAACCTTCGCTCTACCTTACTGGAAGTGGGATAACCCCTACTGGAATGGTTATT
TTACTAGGTTGAAAGCGAGATGGAATGACCTTGACCCCTATTGGGATGACCTTACCAATAA
N D P T F A L P Y W N W D N P T G M V I

781-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+840
CCTGCCATGTTCGAACACAGAACAGCAAACTAACTCTCTGTTTGACCCCTTTAAGGGATGCG
GGACGGTACAAGCTTGCTCTTGCTGTTTGAATTGAGAGACAAACTGGGAAATTCCTTACGC
P A M F E Q N S K T N S L F D P L R D A

841-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+900
AAACACCTCCACCTTCTATCTTTGATGTTGAATATGCTGGTGCAGACACTGGTGCCACT
TTTGTGGAGGTTGAAGATAGAAACTACAACCTTATACGACCACCGTCTGTGACCACCGTGA
K H L P P S I F D V E Y A G A D T G A T
```

FIGURE 15D

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TGTATAGACCAGATAGCCATTAACTGTCTTCAATGTACAGACAGATGGTCACCAACTCC
901-----+-----+-----+-----+-----+-----+-----+960
ACATATCTGGTCTATCGGTAATTAGACAGAAGTTACATGTCTGTCTACCAGTGGTTGAGG
C I D Q I A I N L S S M Y R Q M V T N S

ACTGATACAAAACGATTCTTCGGTGGCGAATTGTAGCTGGAAATGACCCTCTTGGGAGC
961-----+-----+-----+-----+-----+-----+-----+1020
TGA CTATGTTTGTAAAGAGCCACCGCTTAAACATCGACCTTTACTGGGAGAACGCTCG
T D T K R F F G G E F V A G N D P L A S

GAGTTCAACGTAGCTGGACCGTAGAAGCTGGGGTTCACACTGCGGCTCACCGCTGGGTG
1021-----+-----+-----+-----+-----+-----+-----+1080
CTCAAGTTGCATCGACCCCTGGCATCTTCGACCCCAAGTGTGACGCCGAGTGGCGACCCAC
E F N V A G T V E A G V H T A A H R W V

GGTAATTCTAGGATGGCCAACAGCGAAGACATGGGGAACCTTCTACTCCGCAGGATATGAT
1081-----+-----+-----+-----+-----+-----+-----+1140
CCATTAAGATCCTACCGGTTGTGCGTTCTGTACCCCTTGAAGATGAGGCGTCCCTATACTA
G N S R M A N S E D M G N F Y S A G Y D

CCTCTCTTTTACGTCCACCATGCGAATGTCGACAGGATGTGGCAAATCTGGAAAGATATT
1141-----+-----+-----+-----+-----+-----+-----+1200
GGAGAGAAAATGCAGGTGGTACGCTTACAGCTGTCCTACACCCGTTTAGACCCTTTCTATAA
P L F Y V H H A N V D R M W Q I W K D I

```


FIGURE 15E

```
1201-----+-----+-----+-----+-----+-----+-----+1260
      GACAAGAGACACACAAGGATCCGACCTCTGGCGACTGGCTAAATGCATCATACGTGTTT
      CTGTTCTTCTGTGTGTTCCTAGGCTGGAGACCGCTGACCCGATTTACGTAGTATGCACAAA
      D K K T H K D P T S G D W L N A S Y V F

1261-----+-----+-----+-----+-----+-----+-----+1320
      TAGGATGAGAATGAAAATCTTGTACGTGTCTACAACCGAGACTGTGTAGACATTAAATCGG
      ATGCTACTCTTACTTTTAGAACAATGCACAGATGTTGGCTCTGACACATCTGTAATTAGCC
      Y D E N E N L V R V Y N R D C V D I N R

1321-----+-----+-----+-----+-----+-----+-----+1380
      ATGGGATATGACTACGAAAGGTCAGCAATCCCATGGATCCGTAGTCGGCCGACTGCACAT
      TACCCTATACTGATGCTTTCCAGTCGTTAGGGTACCTAGGCATCAGCCGGCTGACGTGTA
      M G Y D Y E R S A I P W I R S R P T A H

1381-----+-----+-----+-----+-----+-----+-----+1440
      GCGAAGGGGCGAACGTTGCTGCTAAGTCTGCTGGAATCGTGCAGAAGGTGGAGGATATC
      CGCTTCCCCCGCTTGCAACGACGATTTCAGACGACCTTAGCACGTCTTCCACCTCCTATAG
      A K G A N V A A K S A G I V Q K V E D I

1441-----+-----+-----+-----+-----+-----+-----+1500
      GTATTCGCGTGAAGTTAAACAAGATAGTGAAGGTTCTAGTGAAGGCCAGCTACAAAC
      CATAAGGGCGGACTTCAATTTGTTCTATCACTTCCAAGATCACTTCTCCGGTCGATGTTG
      V F P L K L N K I V K V L V K R P A T N
```

FIGURE 15F

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AGGACCAAGGAGGAAAGGAGAAAGCAAATGAGCTGTTGTTCTGTAATGGAATCACGTTT
1501-----+-----+-----+-----+-----+-----+-----+1560
TCCTGGTTCCCTCCCTTTCCCTCTTTTCGTTTACTCGACAACAAGCACTTACCTTAGTGCAAA
R T K E G K E K A N E L L F V N G I T F

GATGCTGAGCGGTTTCTAAAGATTGACGTGTTTGTCAACGACGTCGACGATGGAATTTCAG
1561-----+-----+-----+-----+-----+-----+-----+1620
CTACGACTCGCCAAAGATTTCCTAACTGCACAAACAGTTGCTGCAGCTGCTTACCTTAAGTC
D A E R F L K I D V F V N D V D D G I Q

ACCACCGCTGCTGATAGTGAGTTTGCTGGTAGTTTCGCACAGTTGCCACATAACCATGGC
1621-----+-----+-----+-----+-----+-----+-----+1680
TGGTGGCGACGACTATCACTCAAACGACCATCAAAGCGTGTCAACGGTGTTTGGTACCG
T T A A D S E F A G S F A Q L P H N H G

GACAAGATGTTTATGAGGAGTGGGGCAGCGTTCGGGATCACGGAGCTCTTGGAAGACATT
1681-----+-----+-----+-----+-----+-----+-----+1740
CTGTTCTACAAATACTCCTCACCCCGTCGCAAGCCCTAGTGCCCTCGAGAACCTTCTGTAA
D K M F M R S G A A F G I T E L L E D I

GAAGCTGAAGGTGATGACTCTGTTGTTGTGACATTGGTGCCGAGAACAGGGTGTGATGAA
1741-----+-----+-----+-----+-----+-----+-----+1800
CTTCGACTTCCTACTACTGAGACAACAACACTGTAAACGCGCTCTTGTCCTCCACTACTT
E A E G D D S V V V T L V P R T G C D E

```

FIGURE 15G

1801 GTAACTATTGGCGAGATCAAGATTGAGCTGGTTCCCATTTGTTAAAGTCTATTGAAGTAA+1860
CATTGATAACCGCTCTAGTTCTAAGTCGACCAAGGTAACAAATTTCAAGATAACTTCATT
V T I G E I K I Q L V P I V *

1861 TGCATTTTCAATTGTTCATTAGTAGTATGCATGGGTACGTAAATCTGTTCCGCTGCTGGTTATC+1920
ACGTAAAAGTTAACAGTAATCATACGTACCCCATGCATTTAGACAAAGCGACAGACCAATAG

1921 GAGGATTTTGTGATGTTCTCGTAACCAAAATAAAGGATTGTCTATTCCTATGTTTGGAAATCG+1980
CTCCTAAAAACTACAAGAGCATTTGGTTTATTATTCTTAACAGTAAGGTACAAAACCTTAGC

1981 TGTAACCGCAGGCATGCATATGTTTGATTTGTTATTTTACTTGAAGCACTTCTGTTTTAG+2040
ACATTGGCGTCCGTACGTATACAAACTAACAAATAAAAAATGAACCTTCGTGAAGACAAAAATC

TAAAAAATAAAAAA
2041-----+----- 2057
ATTTTTTTTTTTTTTT